

FIGURE 1A

MAJORITY	ATGXXGGCGATGCTTCCCTCTTTGAGCGCAAGGCGCGCTCCTCCTGGTGGAGCGCGCACAGCTGGCGT	
343140	..AG..G.....G.....	70
343140	.....G.....G.....	69
343140	..GA.....A.....	70
MAJORITY	ACCGCACCCTTCTTGGCGCTCAGCGCGCTCAGGACGAGCGCGCGCGCGCTCAGCGCGCTCAGCGCGCT	
343140	.....GA.....G.....	140
343140	.....G.....G.....	137
343140	.....G.....G.....	140
MAJORITY	CGCCAGAGCGCCCTCGTCAAGCGCGCTCAGGAGGAGCGCGGACGXGCGCGCTGCTGCTGCTTTCAGCGCGCAAG	
343140	.....G.....A.....	207
343140	.....A.....G.....	204
343140	.....I...AA...C...CT.....	210
MAJORITY	CGCGCGCTCCTTCCCGCGCAGCGCGCTACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTTC	
343140	.....G..GG.....G.....	277
343140	.....G.....G.....	274
343140	.....G.....G.....	280
MAJORITY	CGCGCGCAGCTCGCGCGCTCATCAAGCAGCTCGTGGAGCTCGTGGCGCTTCGCGCGCGCTCGAGGTCGCGCGCGCTA	
343140	.....A.....G.....	347
343140	.....G.....I.....	344
343140	.....G.....I...A.C.....	350

FIGURE 1B

SEQUENCE	CCACGGCGGACGACCTXCTGGCCACCCCTGGCGAACAAGCGCGGAAAGGAGCGGGTACGACGCTGGCCCATCCTC	417
SEQUENCE	.....C.....G.....C.....	414
SEQUENCE	.....G.....GG.....	420
SEQUENCE	.....T.....G.....	
SEQUENCE	ACCGCGGACCGCGACCTGTACGAGCTCCCTTCGGACCGGCAICGCGGTCCTCCACCCCGAGGGGTACCTCA	487
SEQUENCE	.....AAA.....T.....CA.....	484
SEQUENCE	.....T.....G.....G.....A.....T.....C.....	490
SEQUENCE	.....A.....G.....G.....G.....CC.....	
SEQUENCE	TCGCGCGCGCGCTGGCTTTCGGAGAGTACGCGCGCTGAGCGCGGAGCAGCTGGCTGGACTACCGCGCGCGCTGGC	557
SEQUENCE	.....C.....A.....C.....C.....CC.....A.....	554
SEQUENCE	.....AC.....C.....C.....C.....T.....C.....C.....	560
SEQUENCE	.....A.....C.....C.....C.....C.....C.....C.....	
SEQUENCE	GGCGGACCGCGCTGGGACACCTCCCGCGCGTGAAGGCGCATCGCGGACAGAGCGCGCGCGGACCTCTCXAG	627
SEQUENCE	.....GAG.....T.....G.....GAG.....T.....GG.....	624
SEQUENCE	.....G.....T.....A.....G.....A.....G.....A.....CGC	630
SEQUENCE	.....C.....T.....A.....G.....T.....C.....A.....	
SEQUENCE	CGCTCGCGGACCGCTGGAAAACCTCTCTGAAGAACCTGGACCGCGGCTGAACCGCGC...CXTCGCGGACAGAGA	694
SEQUENCE	.....CG.....G.....A.....A.....T.....T.....C.....	691
SEQUENCE	.....T.....C.....C.....A.....A.....A.....A.....A.....G.....	700
SEQUENCE	.....A.....	

FIGURE 1C

500000	TCGAGCGCGCACAIGGAXGACCTGAXGCCCTCTCTGGGAGGCTTCCGACGCTCCGACCGGACGCTCCGCGCTCGA	764
500010	.....C..T...A.....C...G...A.....	761
500020	.....GCG.....GCG...CCC..I...C..A...I.....A...I.....	770
500030	.....A.....G.....A.....C..G.....I.....C.....C.....C.....	
500040	CGTGGACITCGCGAAGXGCGCGGAGCGCGGAGCGCGGAGCGCGGCTTAGCGGCTTCTCGAGAGCGGCTGGAGCTT	834
500050	.....AA.....A.....A.....A.....A.....I.....I.....	831
500060	.....GG..G..G..G..CACA...A...I.....I...GG...I...I...C..I.....	840
500070	.....C.....C..G.....C.....C.....C.....C.....	
500080	GCGAGCGCTCGTCCAGGAGTTCGGGCTTCGAGAGCGCGGAGCGGCGCTCGAGAGCGGCGGCTCGCGGCGGCG	904
500090	.....T.....AA.....G.....G.....GCGA.....I.....	901
500100	.....A.....C.....C.....C.....C.....C.....	910
500110	CGGAGCGGCGCTTCGTCGGGCTTCTCTTCGCGCGCGCGGAGCGGCGCTTCGCGGCGGAGCTTCGCGGCGTGGC	974
500120	.....T...T.....G.....AAG.....I.....	971
500130	.....T...T.....TC..T.....T.....G.....AAA.....	980
500140	CGCGGCGGAGGCGGCGGCTCCAGCGGCGGCGGAGCGGCGCTTAXGCGGCGCTXAGGAGGCTXAGGAGGCTG	
500150	.....G.....G.....C.....C.....C...G...T..A..AA..C...C.....C.....	1044
500160	.....G.....G.....G.....G.....G.....G.....G.....G.....	1041
500170	.....G.....G.....G.....G.....G.....G.....G.....G.....	1050
500180	.....G.....G.....G.....G.....G.....G.....G.....G.....	

# FIGURE 1D

1114	CGCGGXC1GCTGCCCAAGGAGCGTGGCGCTTTCGGCCCTGAGCGAGCGGCTXGAGCTCXTCGGCCCGGGACG	1114
1111	.....A.....AG.....C.....A.....T.G.....CC.....C.....	1111
1120	.....G..T.....G.....G.....C.....G.....T.C..A.A.....	1120
1127	.....AA.....G.....G.....TC.....G..A.....G.....	1127
1134	.....C.....C.....C.....C.....TC.....G..A.....G.....	1134
1141	.....CGCGGAGTGGAGCGGAGGAXGCGCGGGGACCGGGCCCTCCXTCCGAGAGCGCTGTCXGAGCTXXXGGAG	1141
1148	.....G.....T.....T.....T.....T.....G.....	1148
1155	.....G.....T.....T.....T.....T.....G.....	1155
1162	.....G.....T.....T.....T.....T.....G.....	1162
1169	.....G.....T.....T.....T.....T.....G.....	1169
1176	.....G.....T.....T.....T.....T.....G.....	1176
1183	.....G.....T.....T.....T.....T.....G.....	1183
1190	.....G.....T.....T.....T.....T.....G.....	1190
1197	.....G.....T.....T.....T.....T.....G.....	1197
1204	.....G.....T.....T.....T.....T.....G.....	1204
1211	.....G.....T.....T.....T.....T.....G.....	1211
1218	.....G.....T.....T.....T.....T.....G.....	1218
1225	.....G.....T.....T.....T.....T.....G.....	1225
1232	.....G.....T.....T.....T.....T.....G.....	1232
1239	.....G.....T.....T.....T.....T.....G.....	1239
1246	.....G.....T.....T.....T.....T.....G.....	1246
1253	.....G.....T.....T.....T.....T.....G.....	1253
1260	.....G.....T.....T.....T.....T.....G.....	1260
1267	.....G.....T.....T.....T.....T.....G.....	1267
1274	.....G.....T.....T.....T.....T.....G.....	1274
1281	.....G.....T.....T.....T.....T.....G.....	1281
1288	.....G.....T.....T.....T.....T.....G.....	1288
1295	.....G.....T.....T.....T.....T.....G.....	1295
1302	.....G.....T.....T.....T.....T.....G.....	1302
1309	.....G.....T.....T.....T.....T.....G.....	1309
1316	.....G.....T.....T.....T.....T.....G.....	1316
1323	.....G.....T.....T.....T.....T.....G.....	1323
1330	.....G.....T.....T.....T.....T.....G.....	1330
1337	.....G.....T.....T.....T.....T.....G.....	1337
1344	.....G.....T.....T.....T.....T.....G.....	1344
1351	.....G.....T.....T.....T.....T.....G.....	1351
1358	.....G.....T.....T.....T.....T.....G.....	1358
1365	.....G.....T.....T.....T.....T.....G.....	1365
1372	.....G.....T.....T.....T.....T.....G.....	1372
1379	.....G.....T.....T.....T.....T.....G.....	1379
1386	.....G.....T.....T.....T.....T.....G.....	1386
1393	.....G.....T.....T.....T.....T.....G.....	1393
1400	.....G.....T.....T.....T.....T.....G.....	1400

**FIGURE 1E**

1464	CGAGATCCGCGCGGCTCGAGCAGCAGGCTCTCGCGGCTCGCGCGCGCGCGGCTCAACCTCAAGTCCGCGCGAG
1461	CC
1470	AG G T G
1534	CAGCTCGAAACGGTGGCTCTCGCAGCTXGGGCTCGCGGCTCGCGCGCGCGCGAGAGAGCGCGAAGG
1531	A
1540	CG C C G T T C G C C A
1604	CCCGCAGCGCGCGCGGCTCGTGGAGCGGCTXGGXGAGCGCGCGCGCGCGATCGTGGACAAAGTCCCTCCAGTA
1601	C C G C A C C C C
1610	T G A G
1674	CGCGCAGCTCACCAGGCTCAGACAGACAGCTAGATXGACCGGCTCGCGXGCGCTCGTCCACCGCGAGACCGGG
1671	G T G A C G A C
1680	G G A G C
1744	CGCCCTCCACACCGGCTCAACCCAGAGCGCGCGCGCGCGCGCGCGCTAGTACCTCGGACCGCGACCGTCC
1741	A T
1750	C C C C

# FIGURE 1F

[illegible]

# FIGURE 1G

MAJORITY	ACCITGCCAAAGCTCCGGGGCTGCATTGAGAAACCGCTGCAGGAGGGCCAGAGGGGGGGCTACCTGCAGCA	2164
DISCREP	.....	2161
DISCREP	.....G.....C.....G,CC.....T.....	2170
DISCREP	.....A.....A.....A.....C.....A.....	.....
MAJORITY	GGCCTCTCGGGGGGGGGGGCTACCTGCCCGGAGGTCACGGCGGGGCTCAGAGGGGTCGGGGGAGGGGGGGGA	2234
DISCREP	.....G.....A.....AG,G.....C.....	2231
DISCREP	.....T.....	2240
DISCREP	.....AA,AA.....	.....
MAJORITY	GGCCATGGCCCTTCAACATGGCCGTCACAGGGGAGCGGGCGGGGACCTCATGAAGCTGGCCCATGGTGAAGCTG	2304
DISCREP	.....	2301
DISCREP	.....G.....	2310
DISCREP	.....	.....
MAJORITY	TTCGGCGGGCTXCAGGAAATGGGGGGCCAGCATGCTTCCTXCAGGTCACAGGAGGCTGCTCC1CGAGGGGGG	2374
DISCREP	.....A.....GG.....	2371
DISCREP	.....I.....G.....T,G.....G.....	2380
DISCREP	.....C.....C.....G.....C.....	.....
MAJORITY	CCAAAGAGCGGGGGGAGCGGCTGGCGGCTTGGCCAGGAGGAGGTCATCGAGGGGGTCTATCCCGCTGGCGGGT	2444
DISCREP	.....A.....A.....CC.....GGG.....G.....	2441
DISCREP	.....G.....G.....AG.....A.....	2450
DISCREP	.....C.....C.....A.....G.....	.....

# FIGURE 1H

5'...3'	GGCCCGTGGAGGCTGGAGGCTGGCGGAGGAGCTGGCTCTGGCGGCAAGGCACTAG	2499
123456789101112131415161718192021222324252627282930313233343536373839404142434445464748495051525354555657585960616263646566676869707172737475767778798081828384858687888990919293949596979899100	.....A.....GA	2496
	.....CC.....	2505
	.....T.....GT....	



FIGURE 2A

WAGGHT	MXAMH PLFEPKORVLLVDCHHLYATRIFFALKOLITSRGEVPVAVYGFAXSLKALKEDG·OAVXVYFDAX	
WAGGHT	RC.....H.....I.....	69
WAGGHT	.....V.....V.....	88
WAGGHT	.....YK.....F.....	70
WAGGHT	APSFRHEAYEAYKAGRAPTPFOFPROLALIKELVOLLCXRLEVPVPGYEADVLATLAKNAEKEGYEVRI L	
WAGGHT	.....S.....	139
WAGGHT	.....A.....	138
WAGGHT	.....V.....F.....R.....	140
WAGGHT	.....FI.....	
WAGGHT	TADRDLYOLLSORIAVLHPGCVLITPAWLWEKYGLRPEQWVDYRALXGDPSPDHLPGVXGIGEXTAXKLLX	
WAGGHT	.....D.....T.....E.....R.....E 209	
WAGGHT	.....Y.....A.....I.....OR.IA 208	
WAGGHT	.....F.....V.....L.....K 210	
WAGGHT	EWGSLERLLKHLDRVKP·XXAREKIXAHMEDLXLSXXLSXVRIOLPLEVGFAXRREPDRGLRAFLELEF	
WAGGHT	.....K.....D.....K.....WD,AK.....K.....R.....	278
WAGGHT	.....L.....D.....K.....WD,AK.....K.....R.....	277
WAGGHT	.....SL.....O.O.....A.A.....AK.....O.H.....GR.T.WL.....	280
WAGGHT	.....ENV.....K.L.....R.....LE.....R.....L.OG.....	
WAGGHT	GSLLHEFOLLXPKALEEAPWPPPECAFVGFVLSRPEPMWAEILLALAAARXGRVHRAXDPLXGLROLKEV	
WAGGHT	.....S.....X.....D.....G.....PE.YXA.....A 348	
WAGGHT	.....G.....A.....L.SF.....O.WE.....L.....O.....R.....G. 347	
WAGGHT	.....A.A.P.....X.....C.D.....A.....A.....K..... 350	

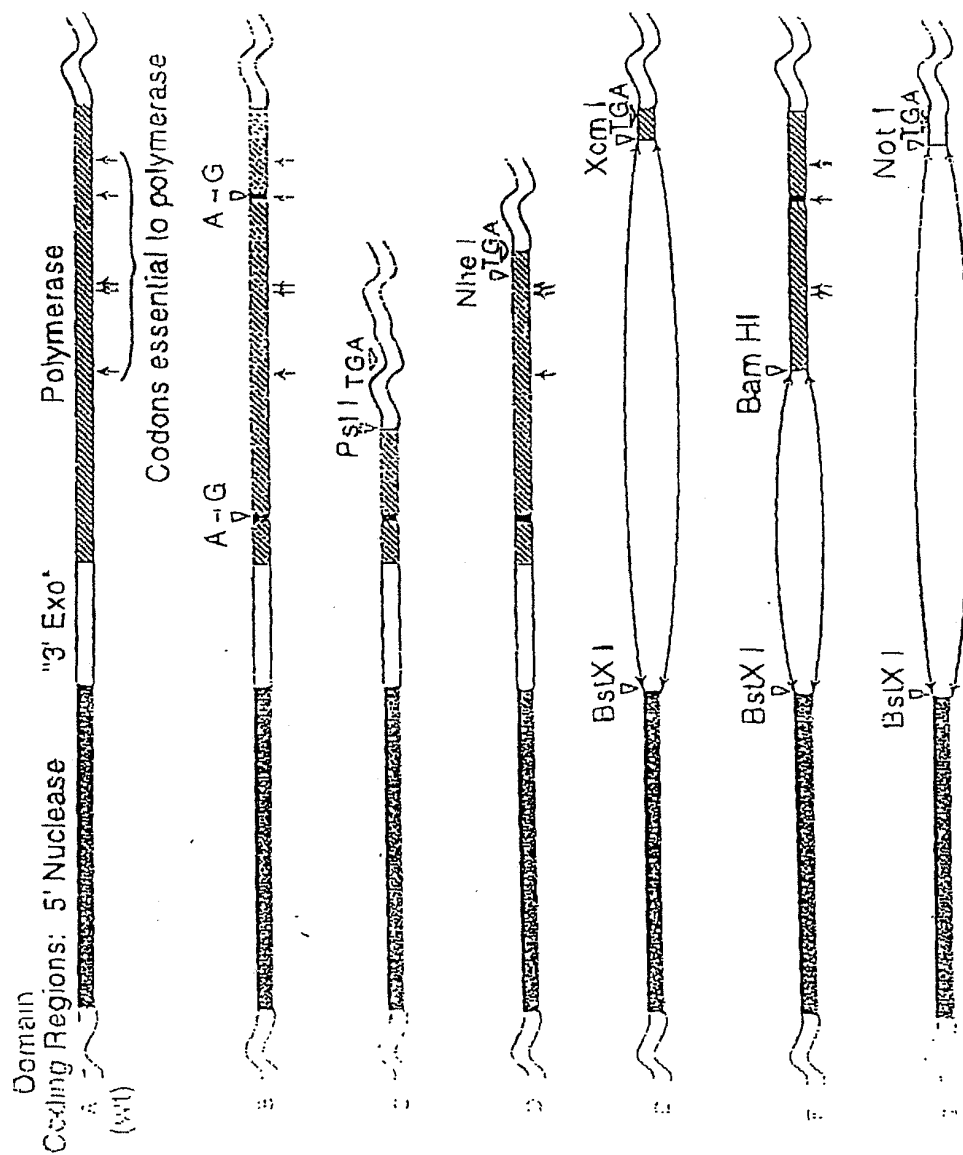
FIGURE 2B

418	AGLIANDLAVLALREGLDLPQDDPHL LAYLLDPSNITPEGVARRYGGEWTEOAGERALLSERLFXHLXX	
419	.....S.....G.P.....E.....A.....A.....WG	418
420	.....I.....F.E.....A.....A.....OI.K	417
421	.....S.....V.....AH.....HA.....LX	420
422	.....K.....	
488	RIECEEELLWLYXEVEKPLSAVLAKMEATGVRLDVAYTLOALSLEVAEEI RRIEEVFRLAOHPFNLSRD	
489	.....R.....A.....A.....R.....A.....A.....	488
490	.....E.....R.....EA.V.O.....EA.V.O.....	487
491	.....K.....K.....L.....L.....	490
558	OLERVLFDELOLPAICKIEKTCKRSTSAAVLEALREAHPIVEKI LOYAEITXIKHTYIDPLPXLVMPRTG	
559	.....R.....L.....O.....S.....O.I.....	558
560	.....A.....L.....O.....OR.....A.....K.....	557
561	.....R.....L.....O.....H.....V.....S.....	560
628	RLRIRFHOTAIATGRISSSDPNLOHVPRTPLQORIRRAFVAEEGWXLVALOYSQIELRVLAHLSDCHL	
629	.....L.....L.....L.....	628
630	.....V.....V.....V.....	627
631	.....A.....A.....A.....	630
698	IRVFOEGRODIHIOTASHWFGVPPPEAVDPLWRAAKTINFGVLVYNSAHRLSQELAI PYEEAVAFIERYFO	
699	.....E.....R.....A.....O.....	698
700	.....S.....S.....G.....G.....S.....	697
701	.....K.....V.....V.....	700

FIGURE 2C

MAJORITY	SFPKVRWIIEXTLEEGRRROYVETLFGRRRYVPOLHARVKSUREAAERMAFNHPVOGTAADLHKLAHVKL	
760 P90	.....E.....	768
765 P90	Y.....G.....	767
770 P90	.....K.....	770
MAJORITY	FPRLXEHGARNLLOVHDEIVLEAPKXAEXVAALAKEVMEGVYPLAVPLEVEVOXGEDWLSAKEX	
830 P90	.....E.....A.....R.....	833
835 P90	.....O.....L.....D.....R.....W.....O.....	831
840 P90	.....R.....L.....O.....A.....E.....A.....KA.....M.....G.....	835

**FIGURE 3**



**FIGURE 4**

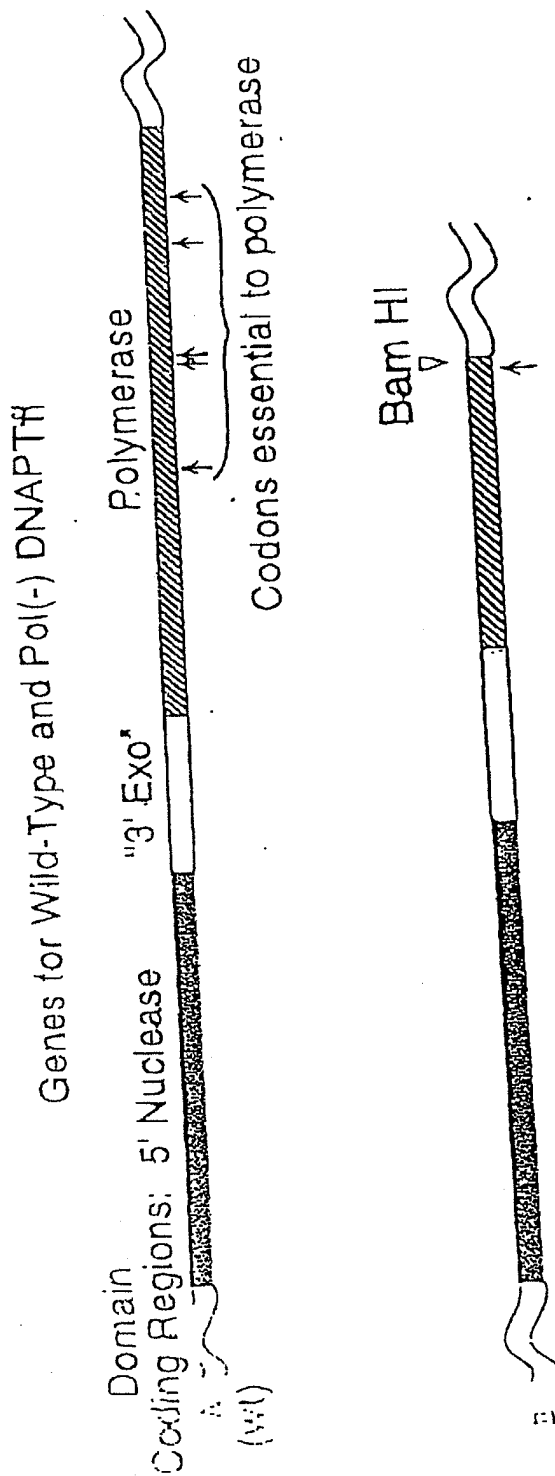


FIGURE 3

5' arm  
TAATACGACTCACTATAGGGAGAC

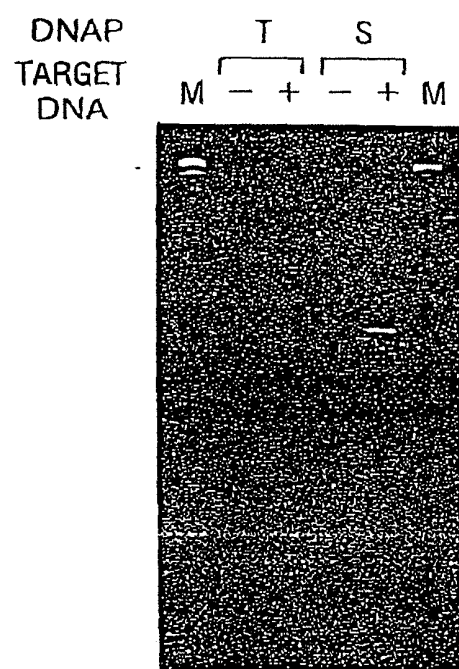
3' arm  
CGGAATTCGAGCTCGC C  
GGCCTTAAGCTCGAGCG G

Substrate Strand

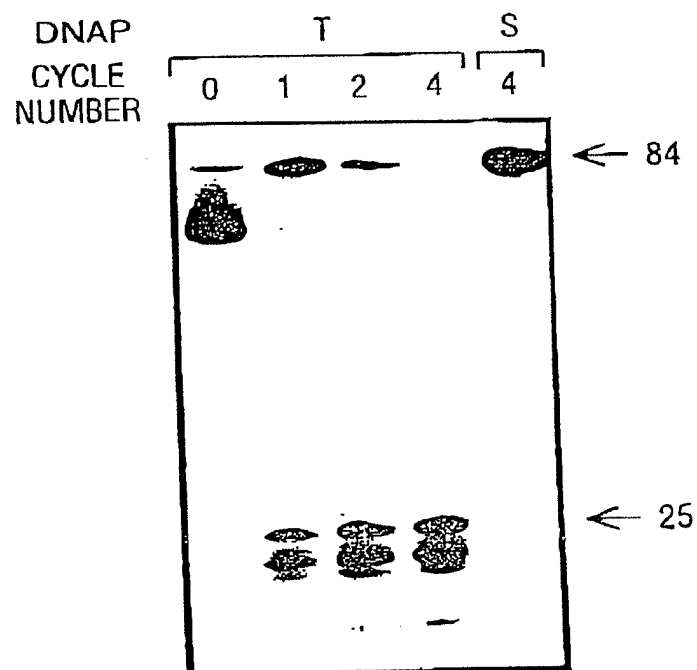
Template Strand

Cleavage Sites  
a b

Primer  
CTTAAGCTAAATCCAGCTGTGATATCTTATGTTAGGCTGACACTATAGAA



**FIGURE 6**



**FIGURE 7**



	1	2	3	4	5	6
DNAP-T:	-	+	+	+	+	+
MgCl <sub>2</sub> :	+	-	+	+	+	+
dNTPs:	+	-	+	-	+	-
Primers:	+	-	+	+	-	-

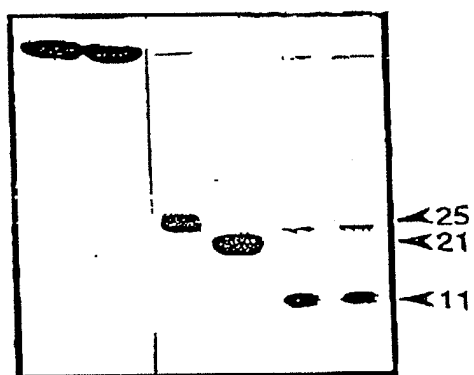


FIGURE 8A

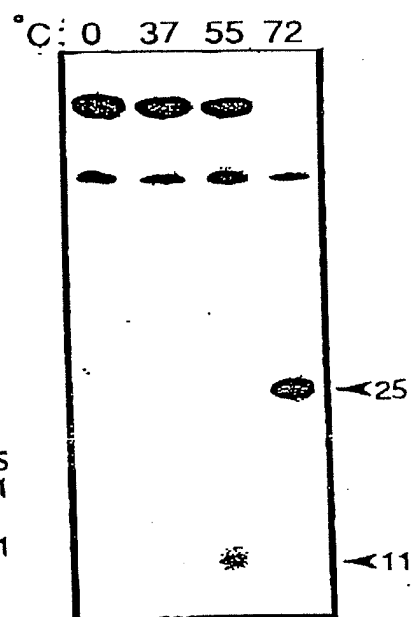


FIGURE 8B

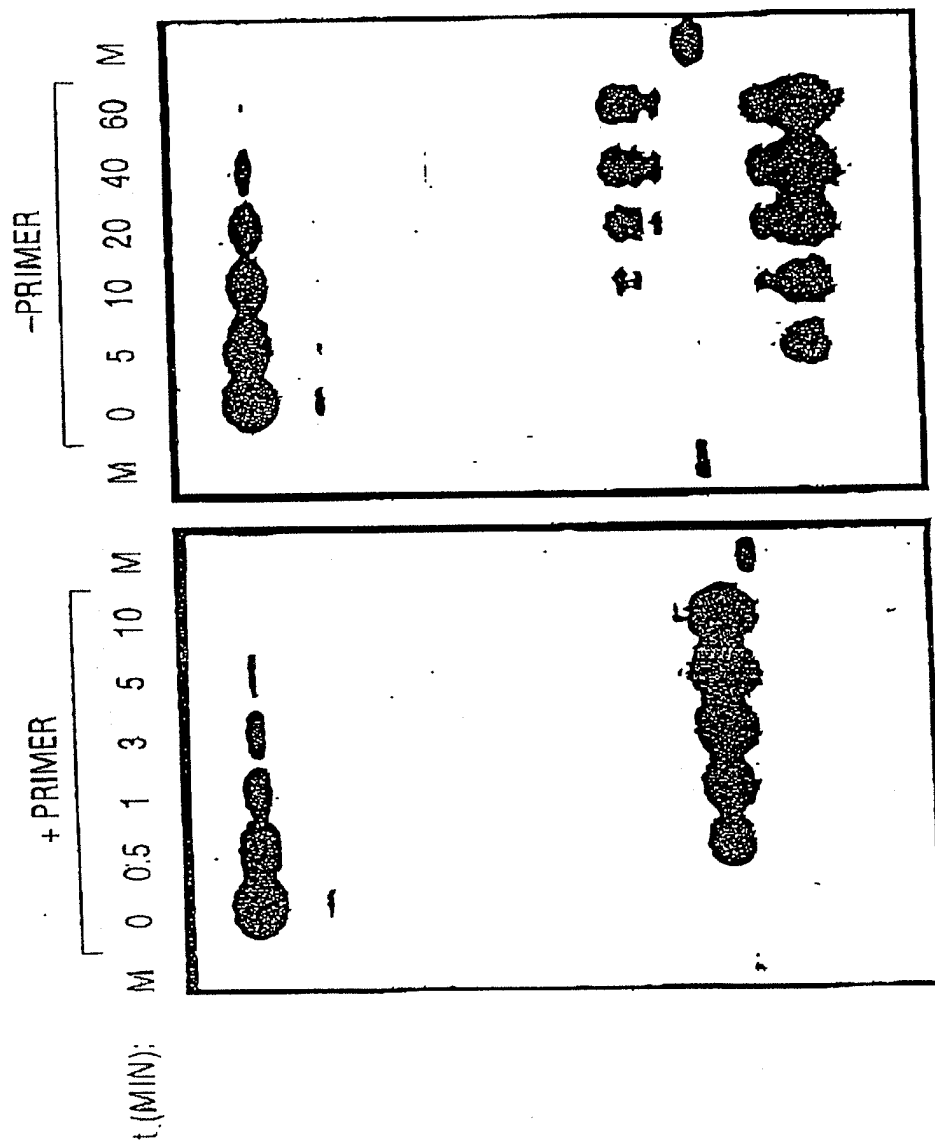


FIGURE 9B

FIGURE 9A

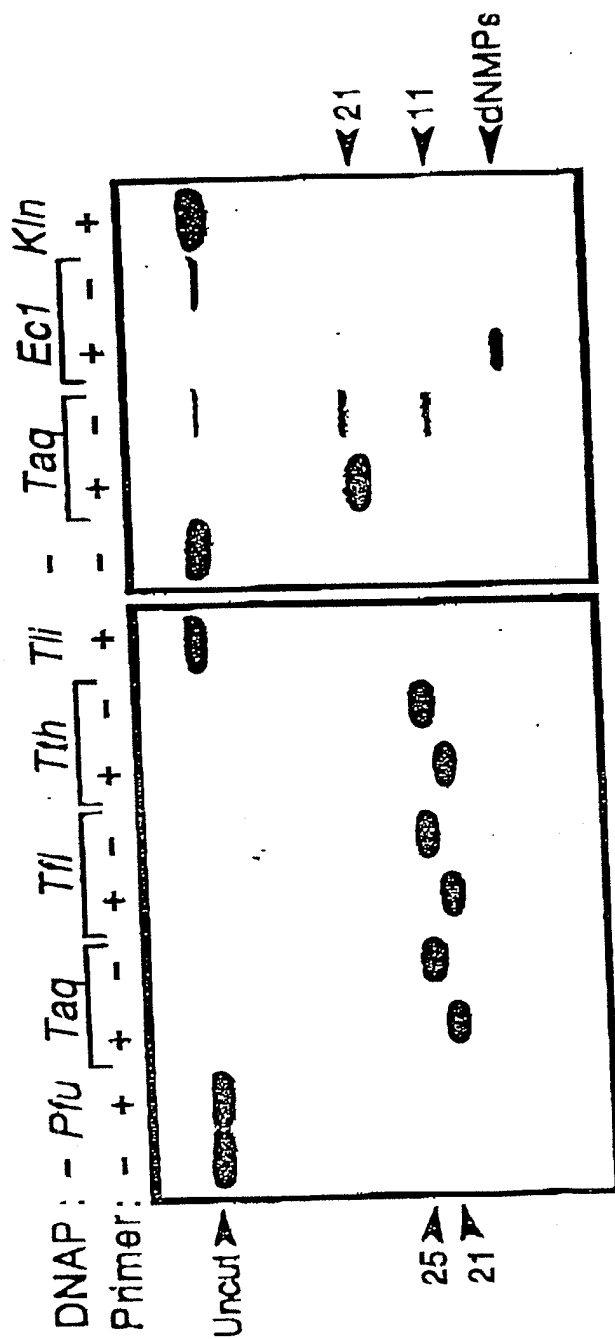
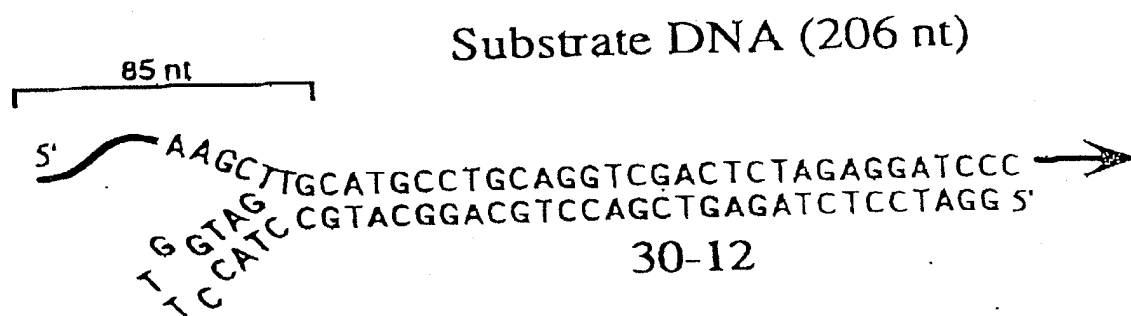
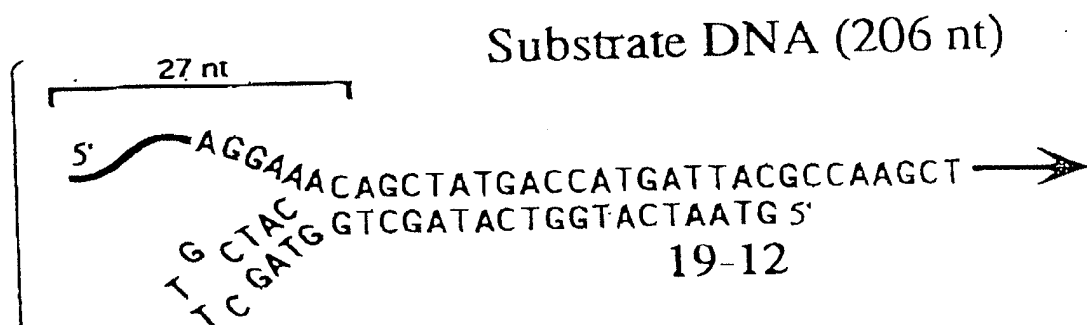
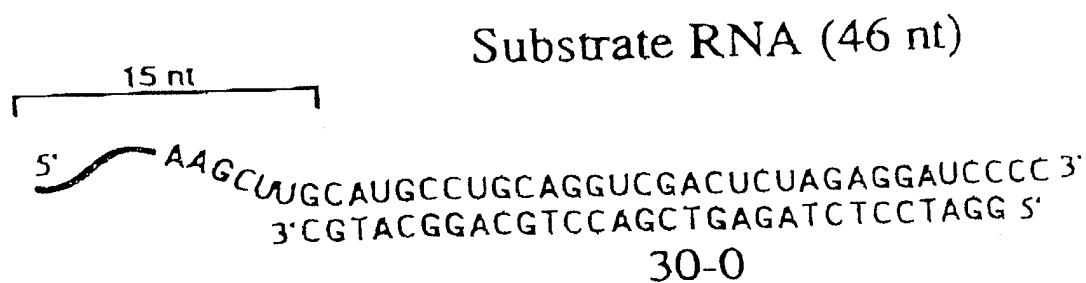


FIGURE 10B

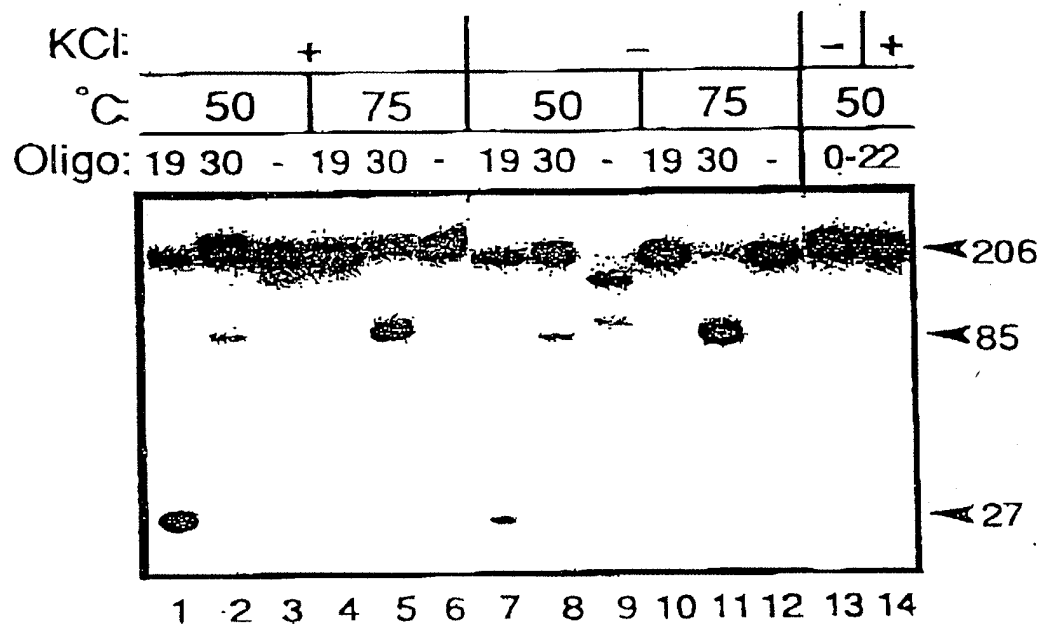
FIGURE 10A



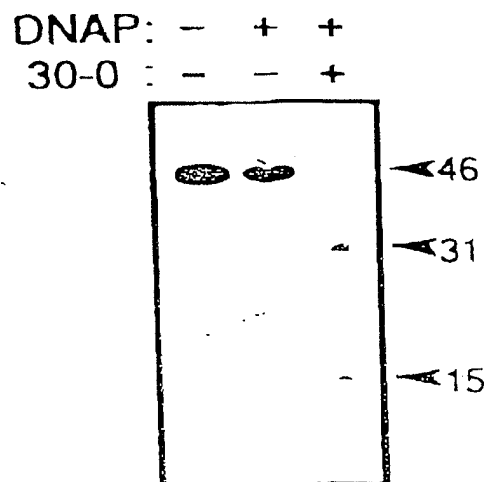
**FIGURE 11A**



**FIGURE 12A**

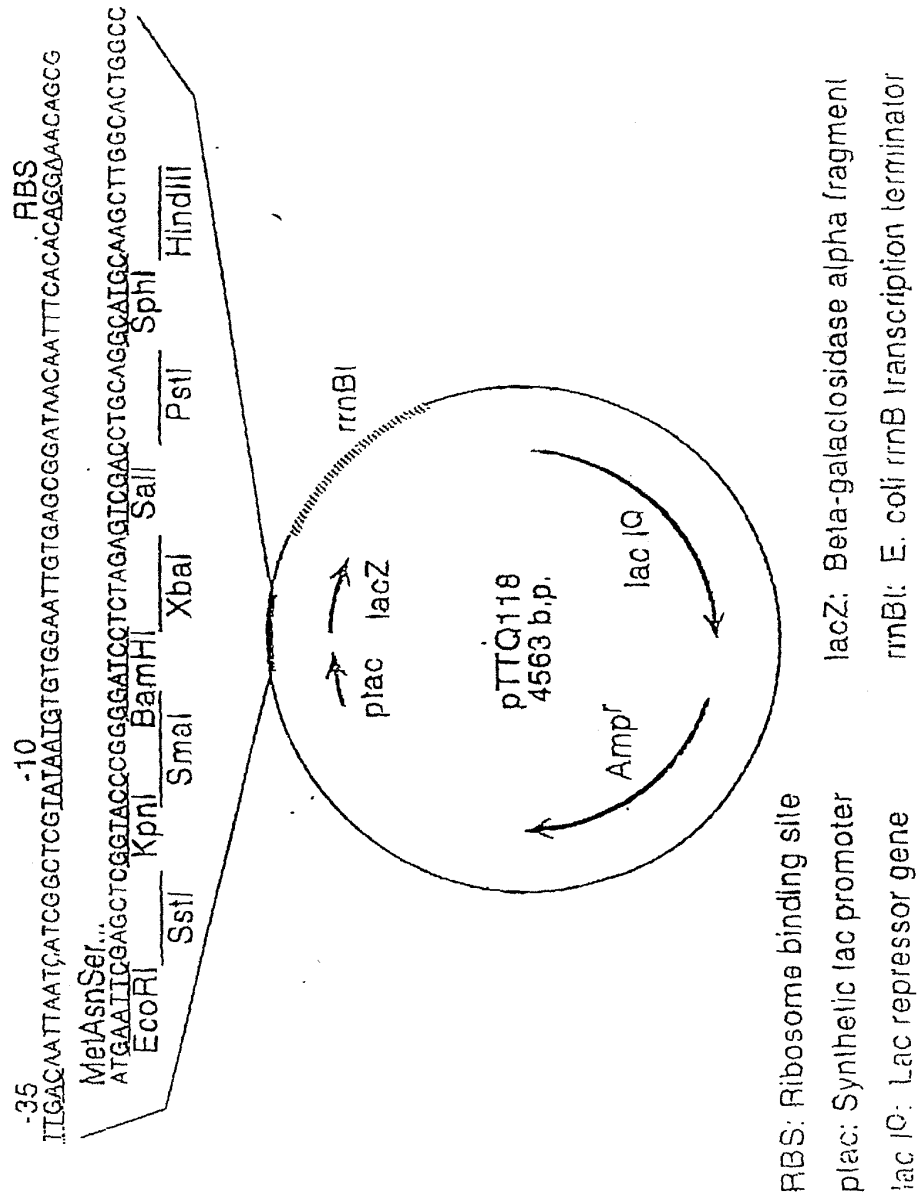


**FIGURE 11B**

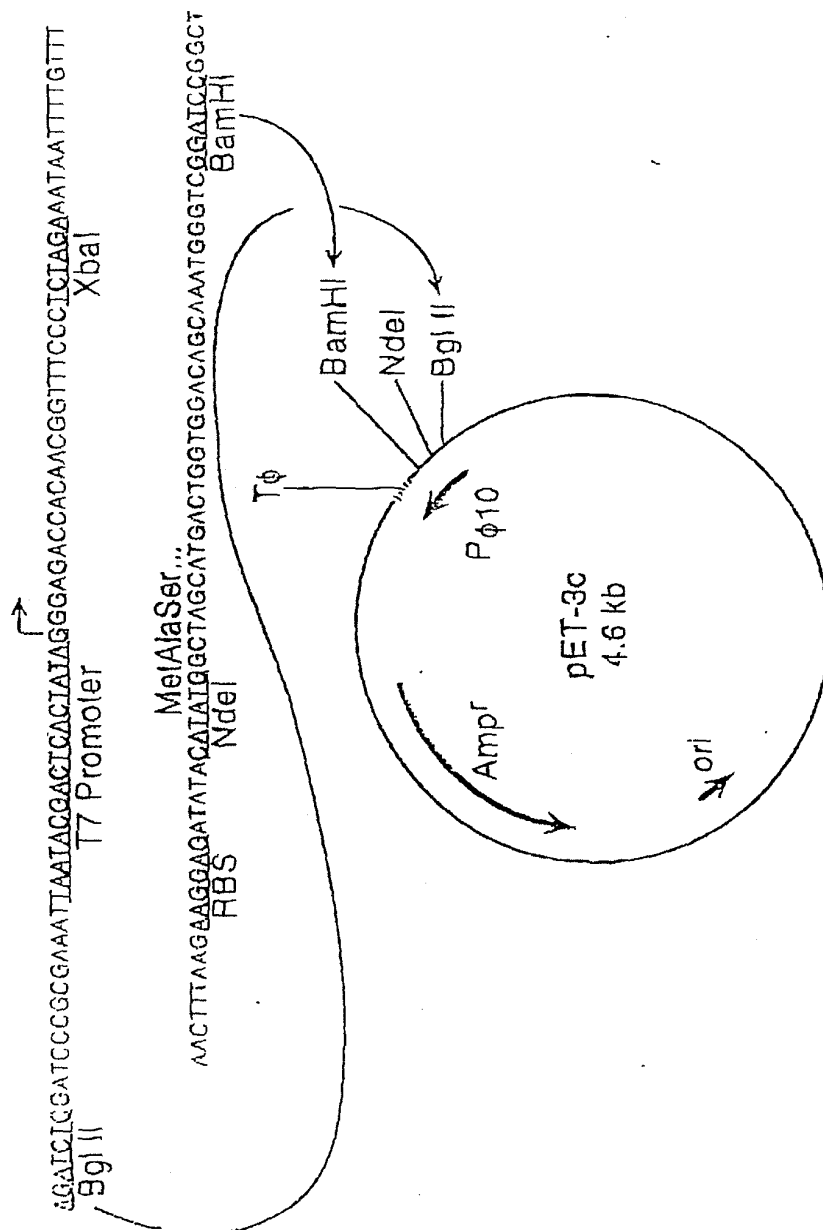


**FIGURE 12B**

FIGURE 13



**FIGURE 14**

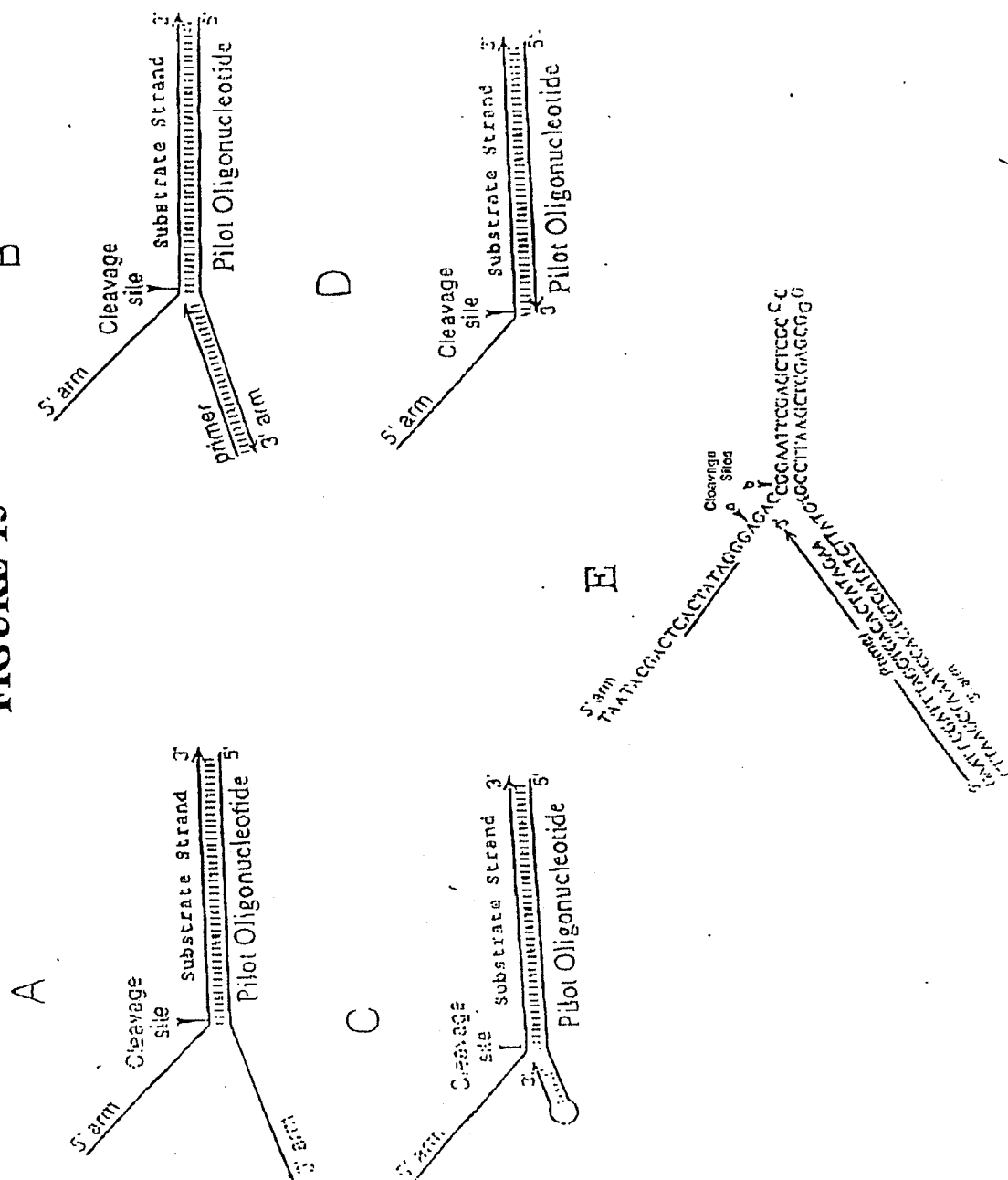


P<sub>φ10</sub>: Bacteriophage T7 φ10 promoter

T<sub>φ</sub>: T7 φ Terminator

RBS: Ribosome binding site

**FIGURE 15**





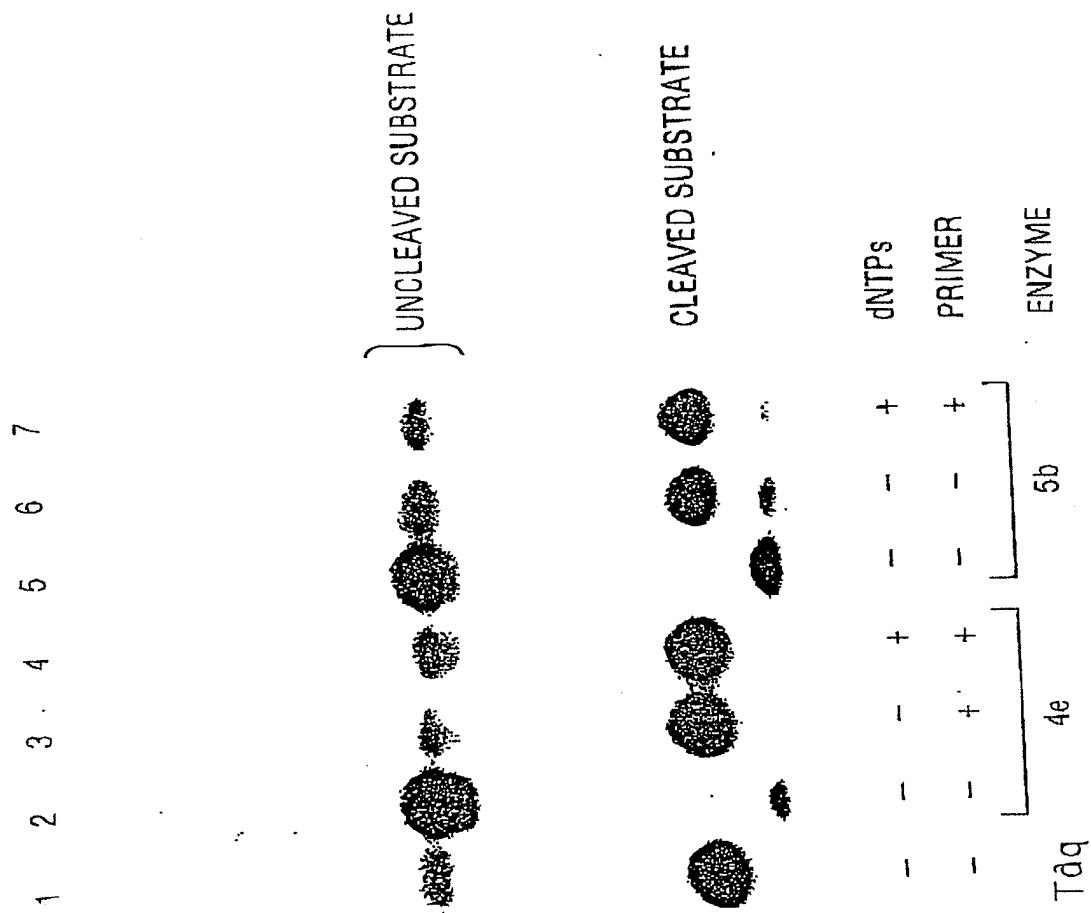


FIGURE 16

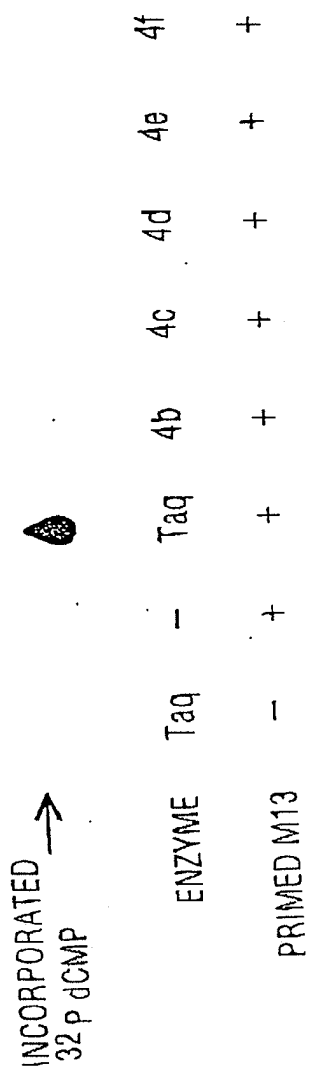
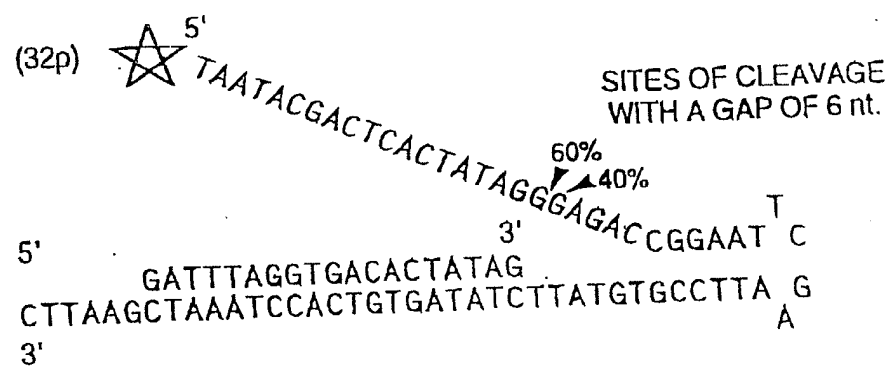


FIGURE 17



**FIGURE 18A**



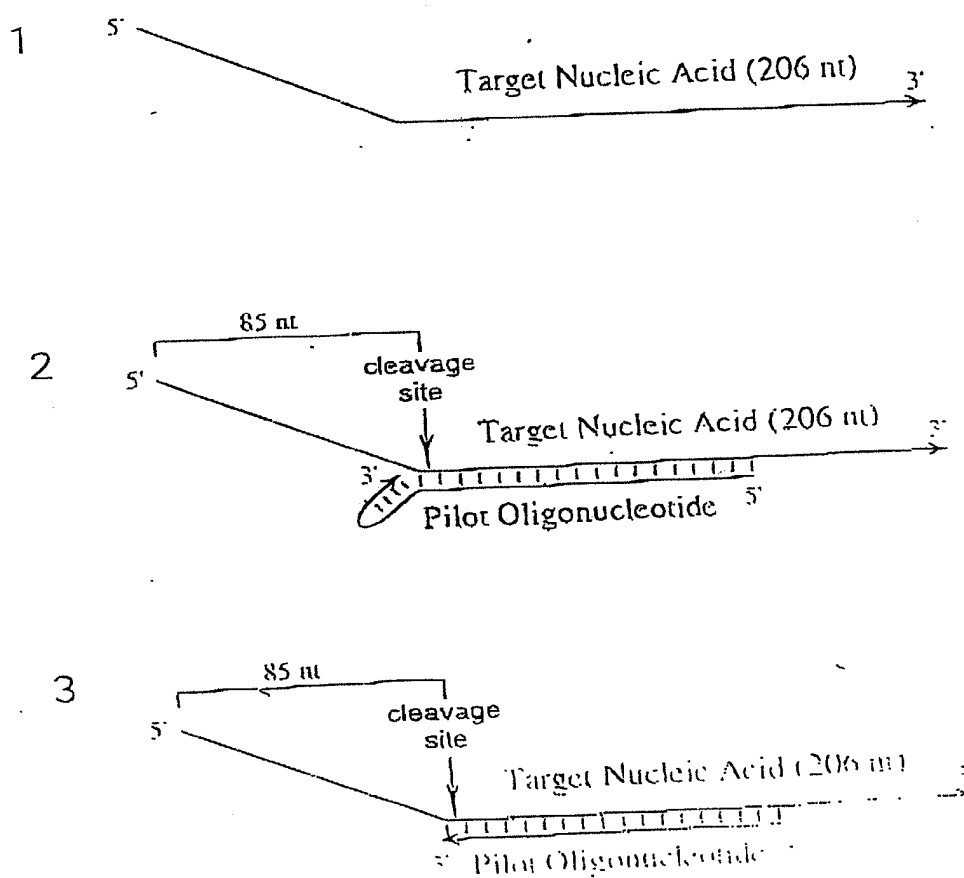
Ban II  
Sst I  
Asp 718  
Ava I  
Kpn I  
Xma I  
Sma I  
EcoR I  
Bam HI XI

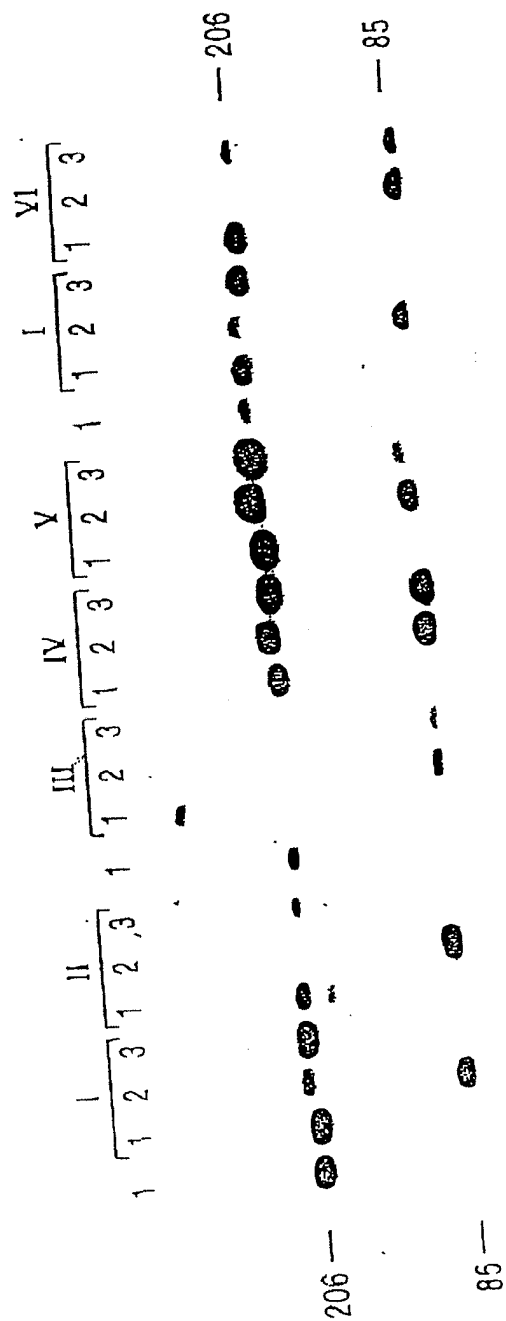
...GACGGAGCTGTAAACGACGCCACTGAATTGTAATAGCACTACTATAGGCAGAAATTCAGGTCGCTACC CGGGAATCC TC  
 ...GCGCCTGCACACTTTTCCCTSCCGCTCACTTAACATTTATCTGAGTGATATCCCGCTTAGCTTCAGGCCATAGGCCCTTAGGAG  
 ...T7  
 Pilot 30-0

[illegible]

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**FIGURE 20A**





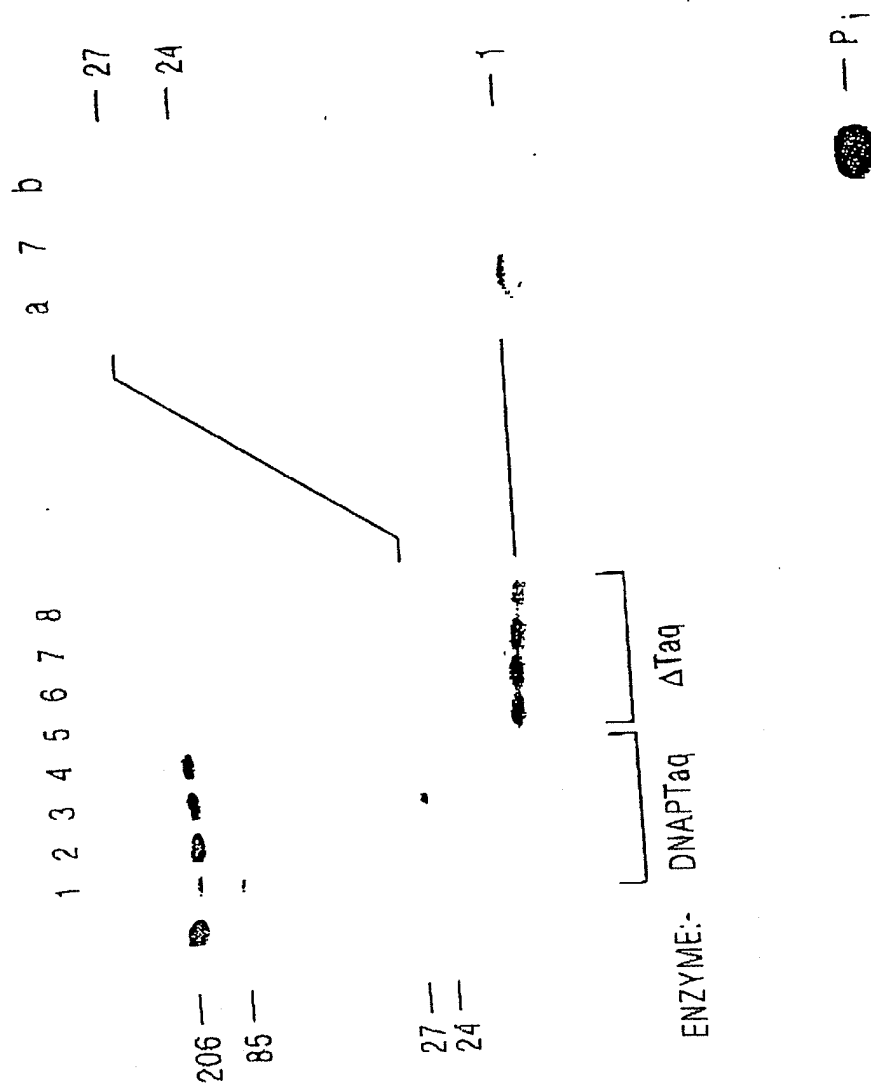


FIGURE 21B

FIGURE 21A



FIGURE 22A



— 206



FIGURE 22B

\* = 32p

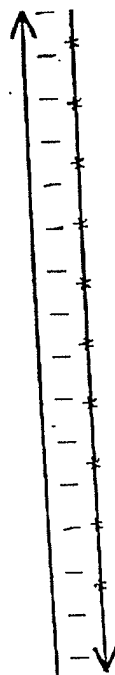
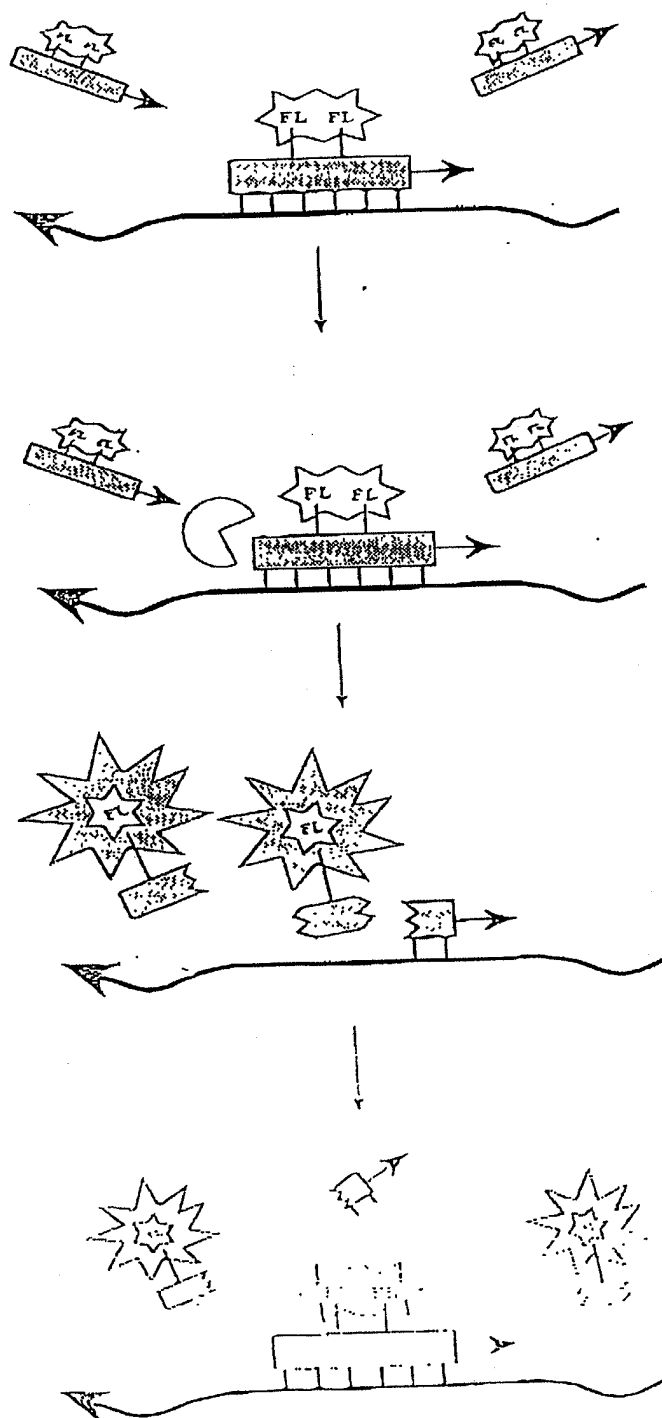
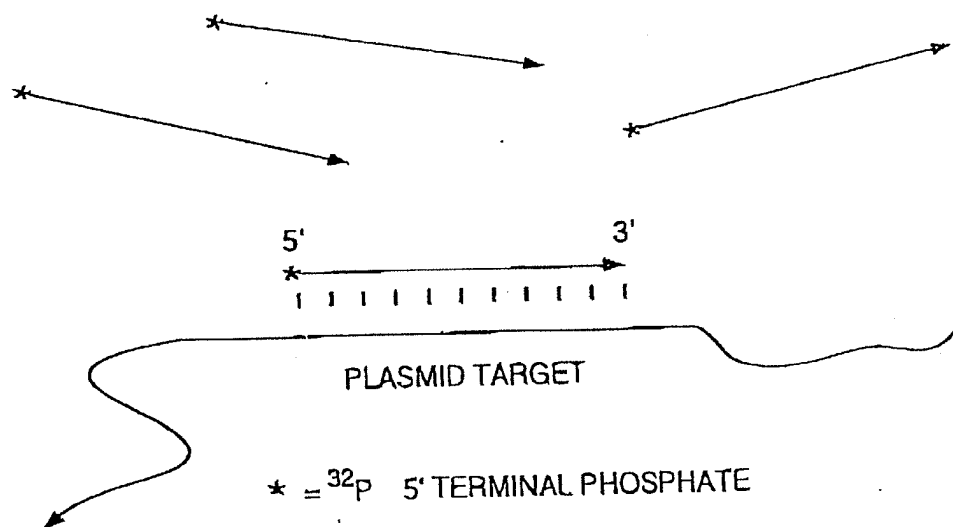


FIGURE 23





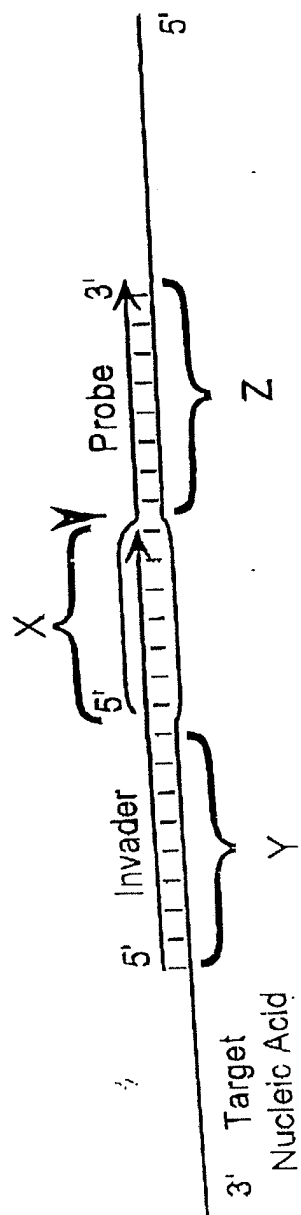
**FIGURE 24A**

M 1 2 3 4 5 6

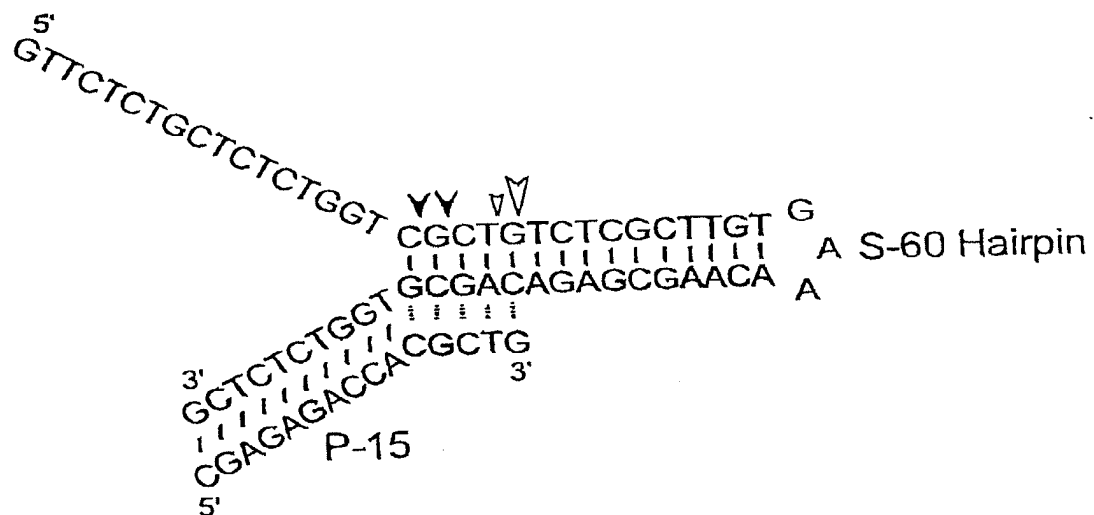


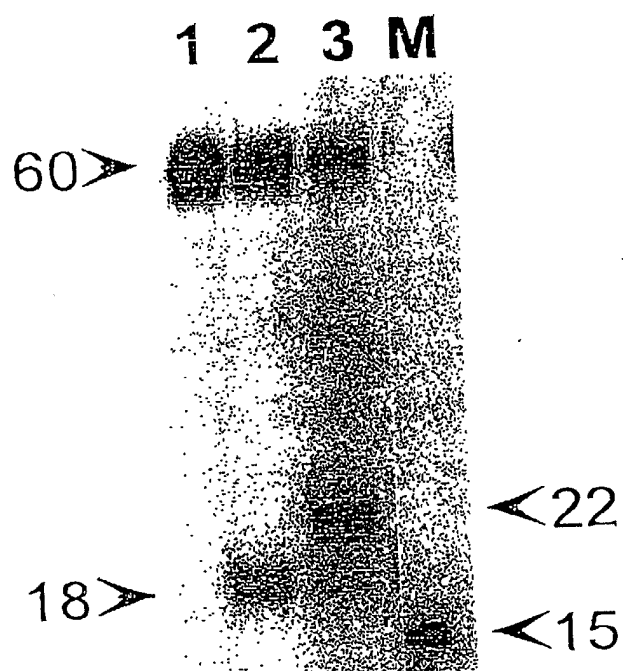
**FIGURE 24B**

FIGURE 25



**FIGURE 26**





**FIGURE 27**

FIGURE 28

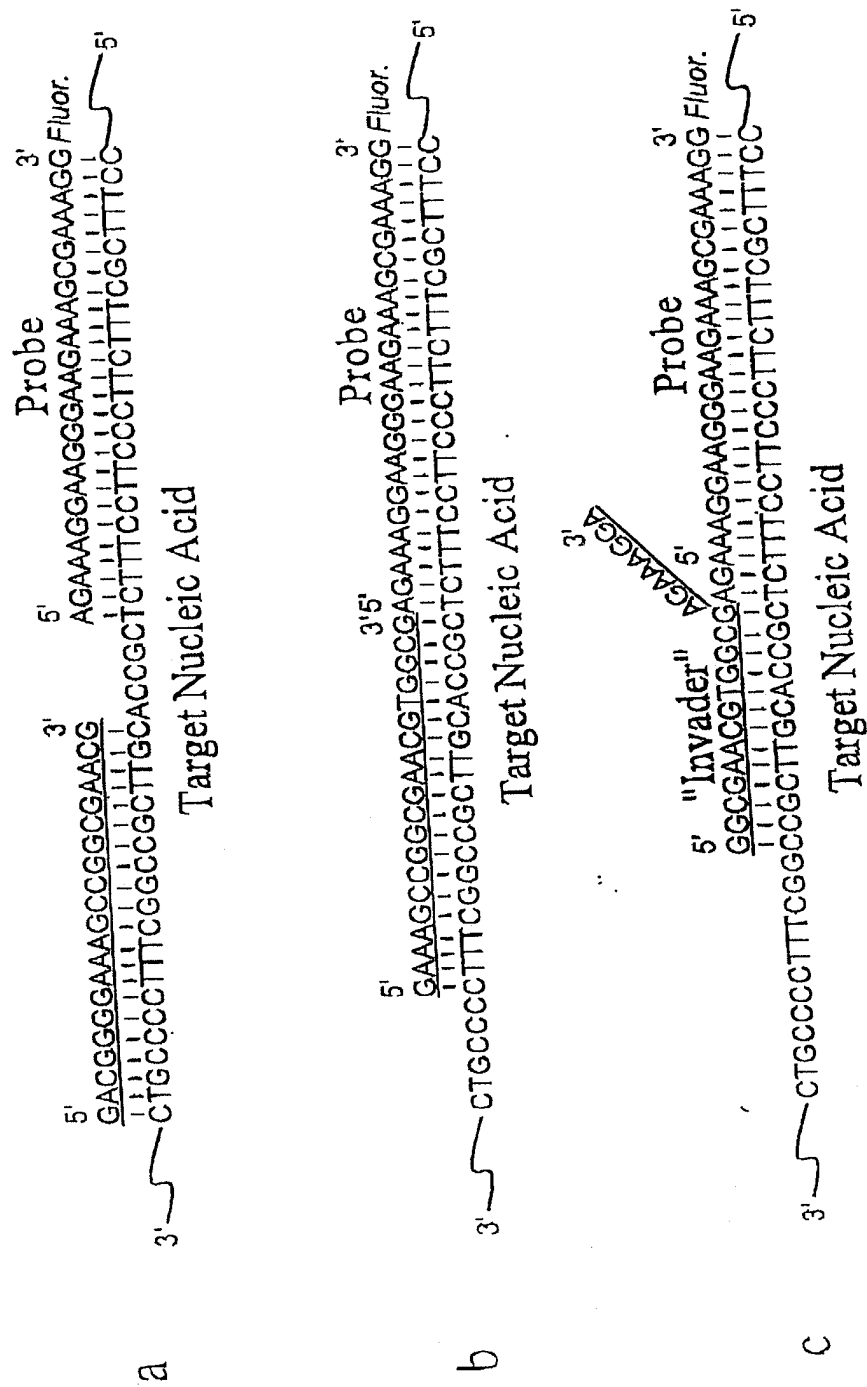
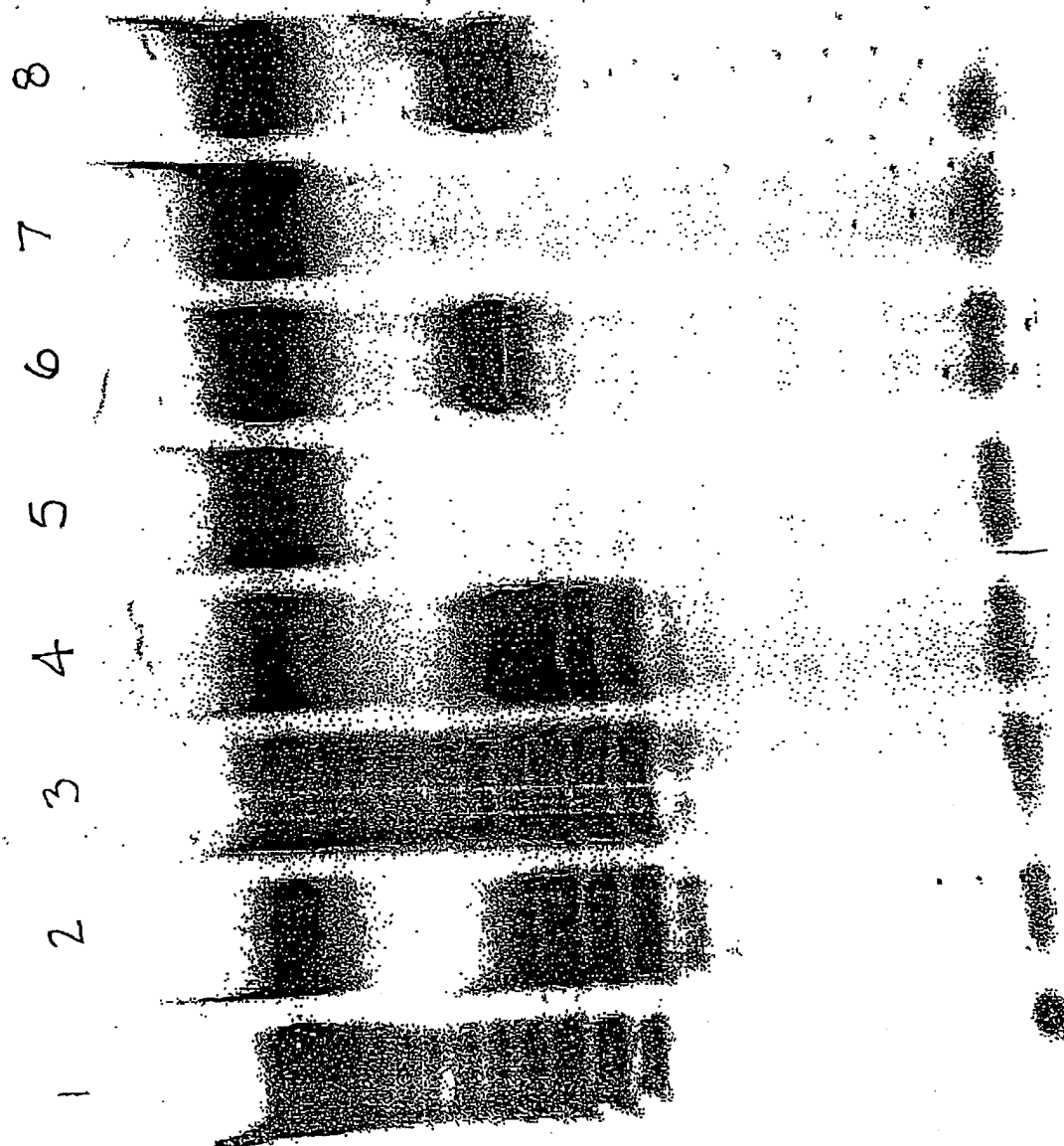




FIGURE 29



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FIGURE 30

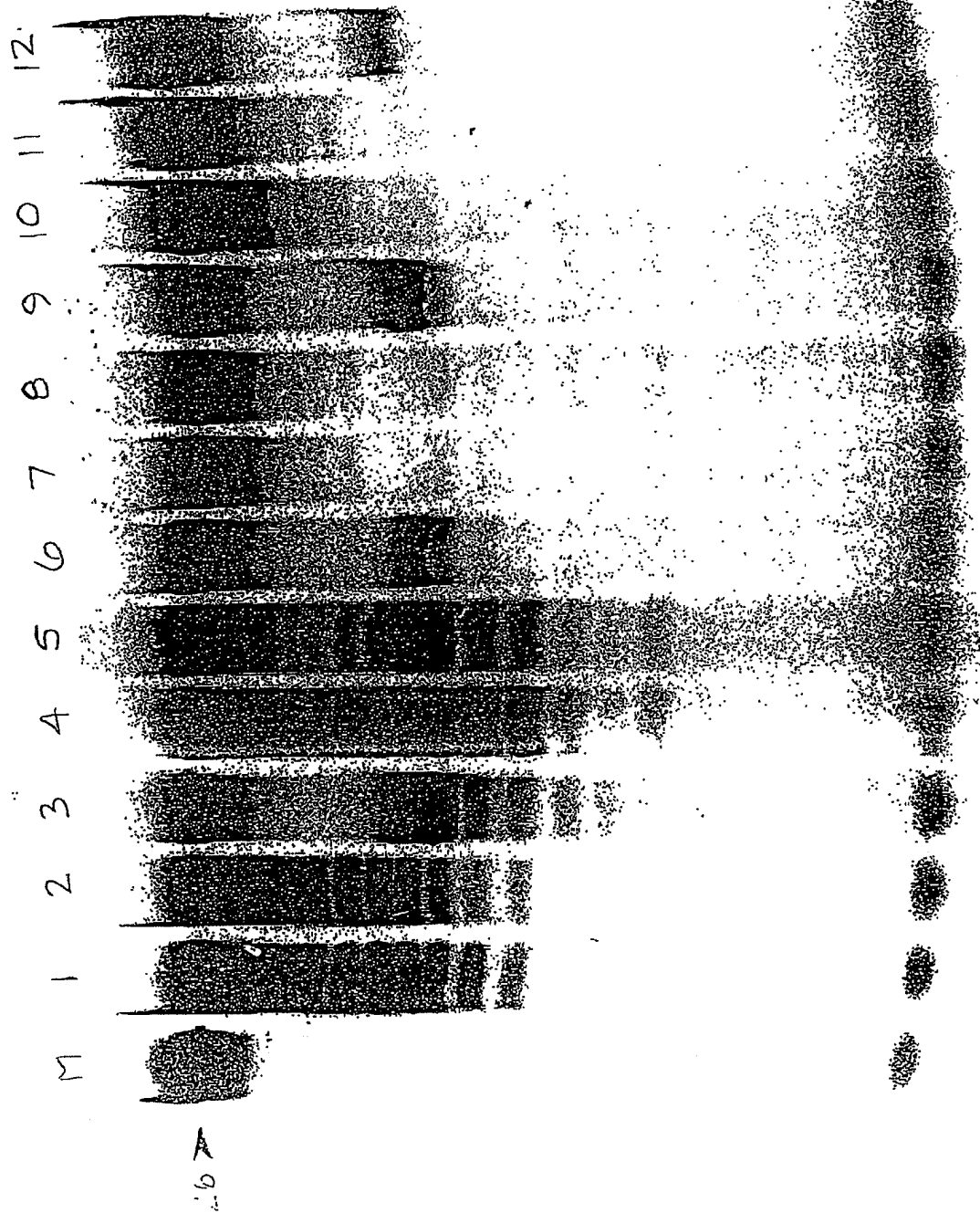


FIGURE 31

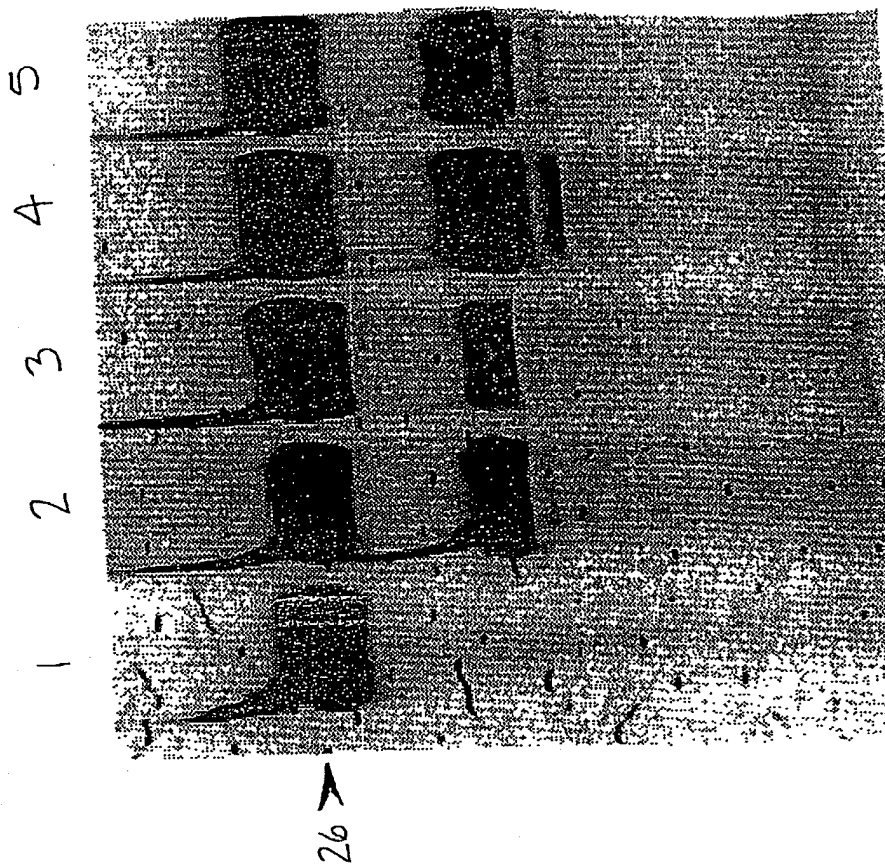


FIGURE 32

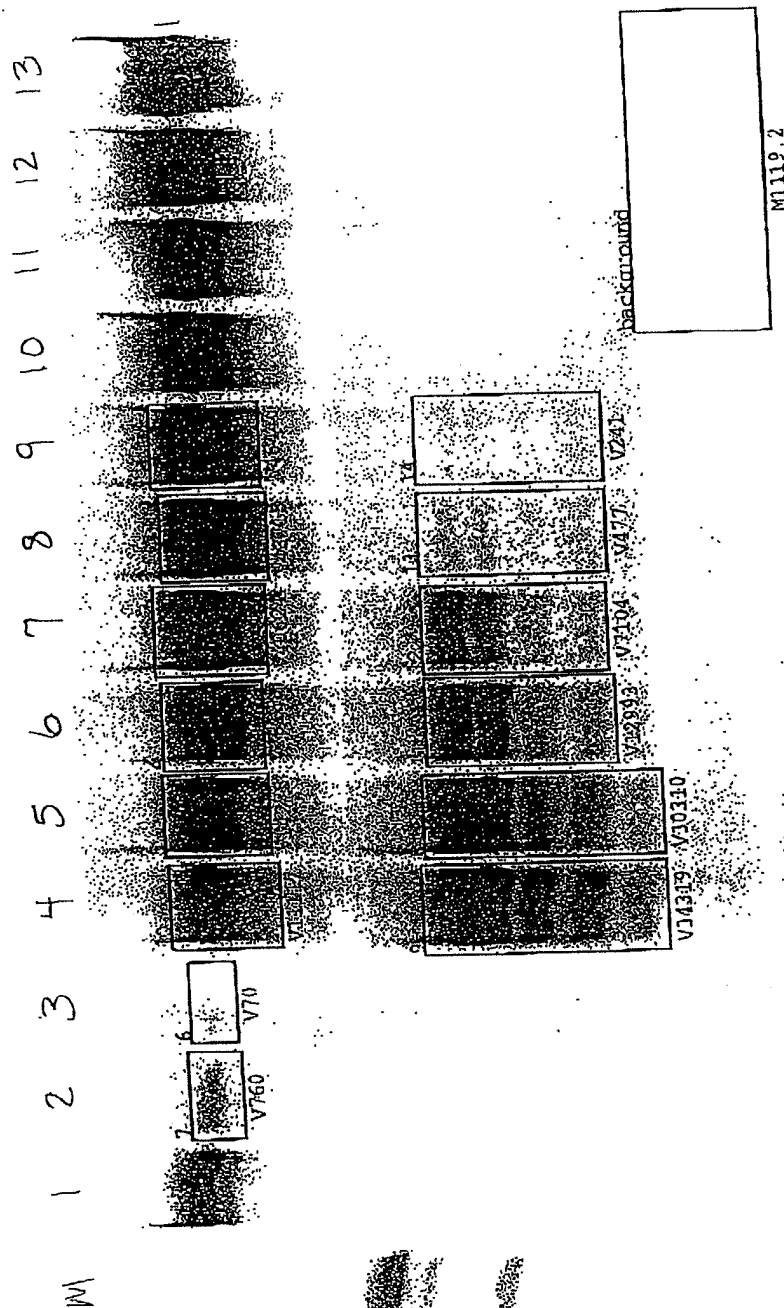


FIGURE 33

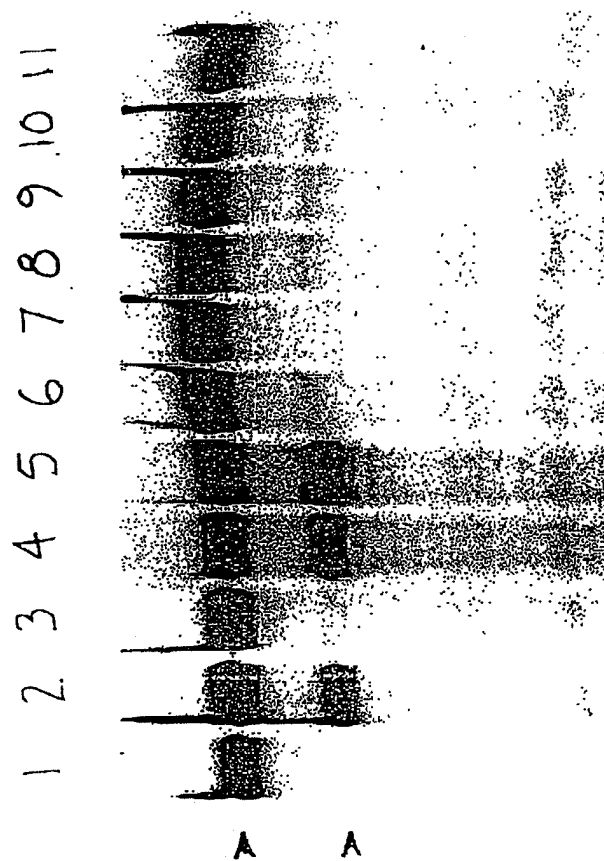
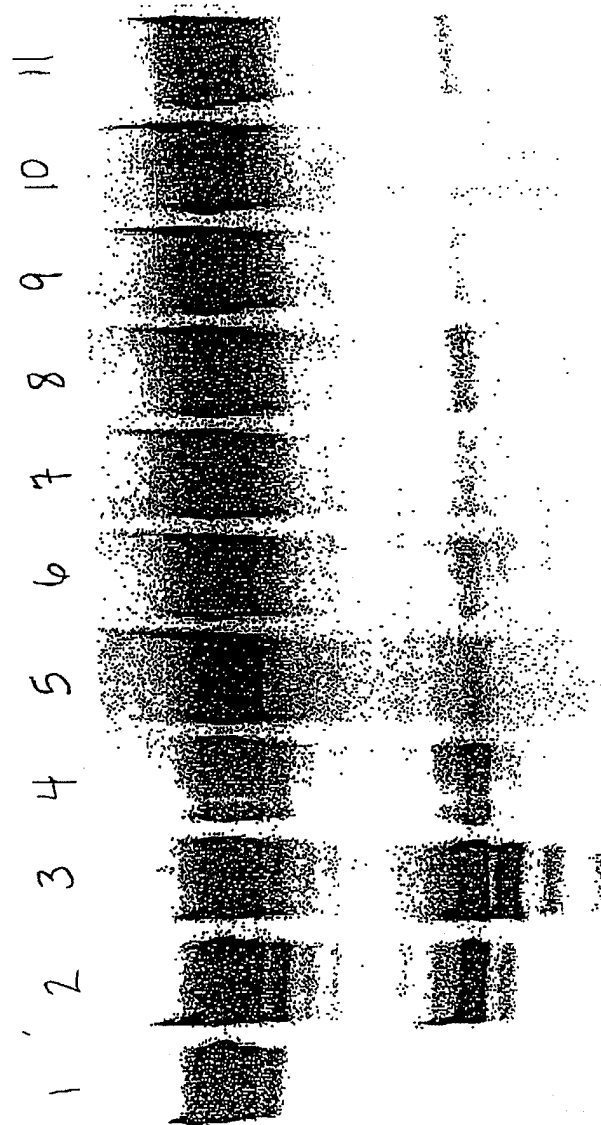
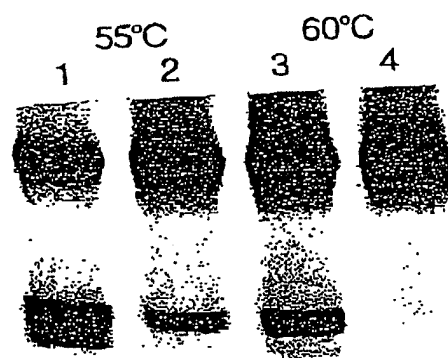
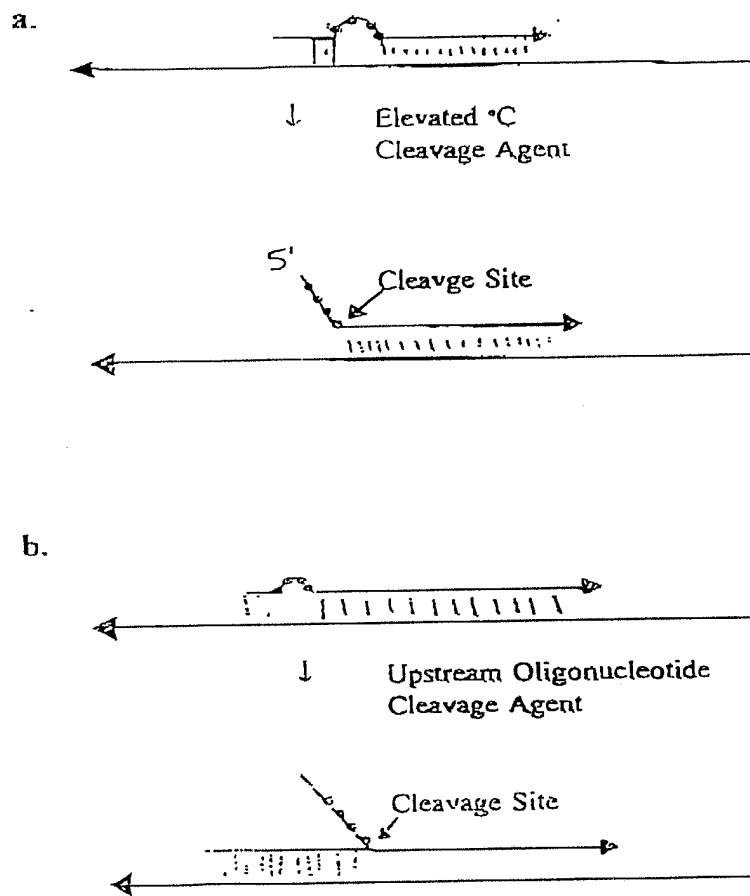


FIGURE 34



**FIGURE 35**



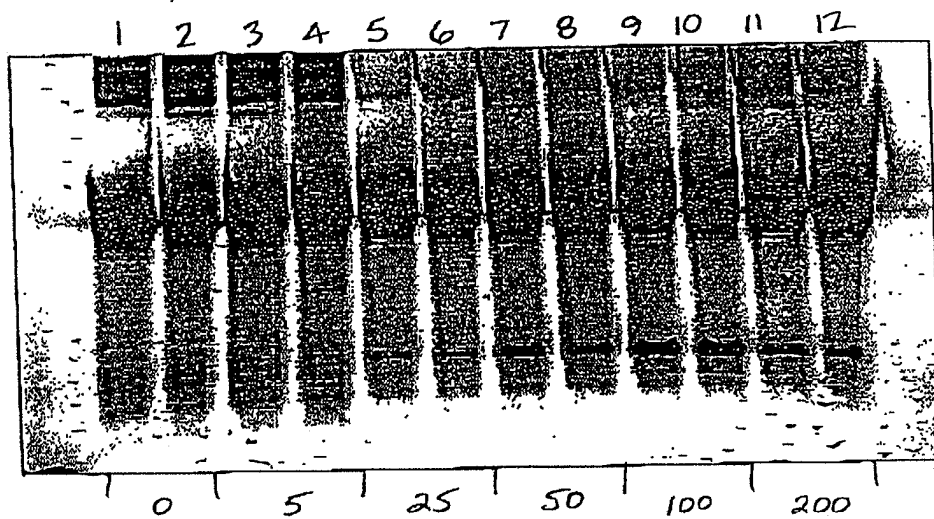


**FIGURE 36**

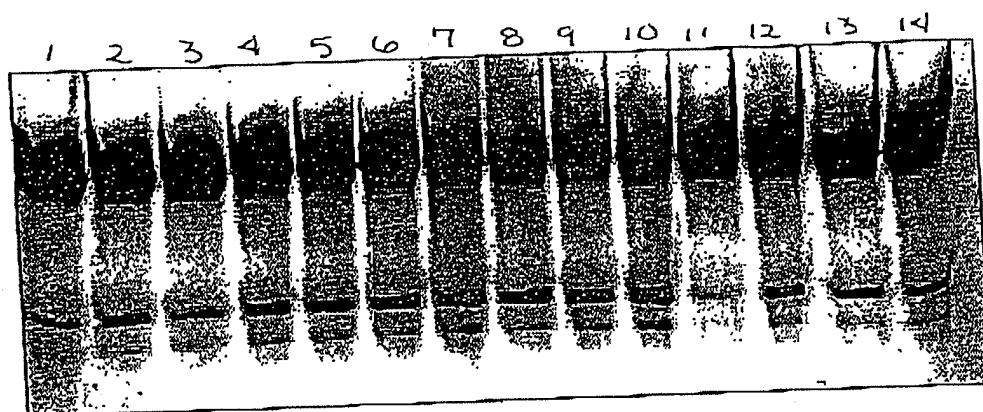




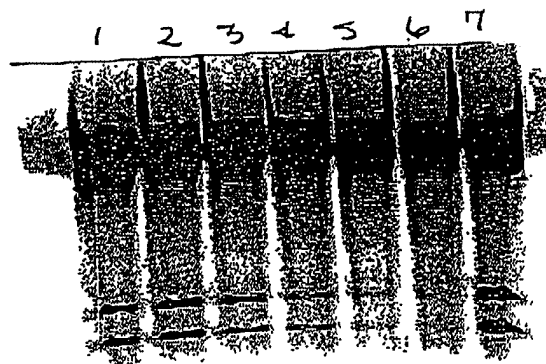
**FIGURE 38**



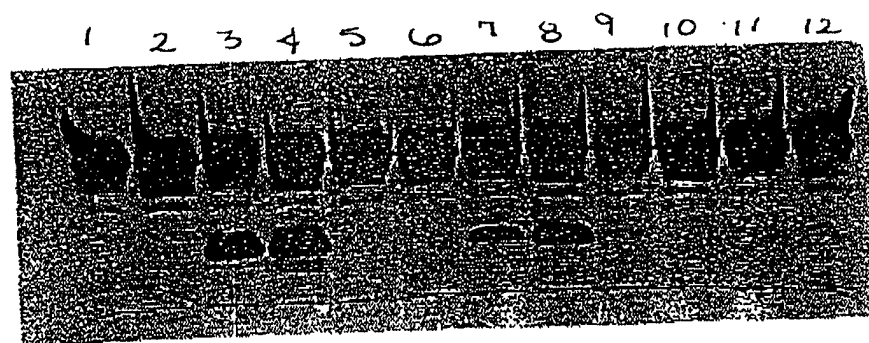
**FIGURE 39**



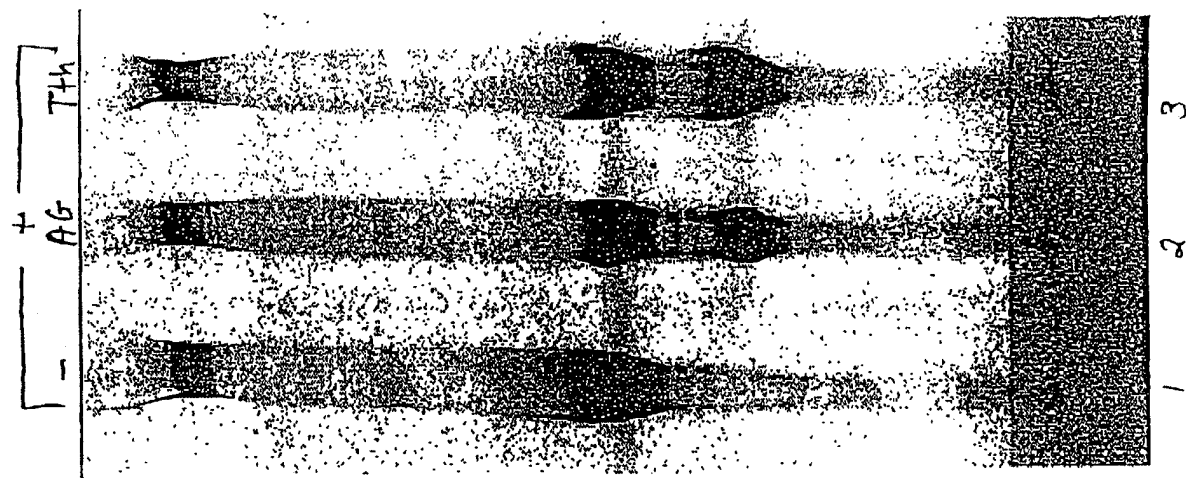
**FIGURE 40**



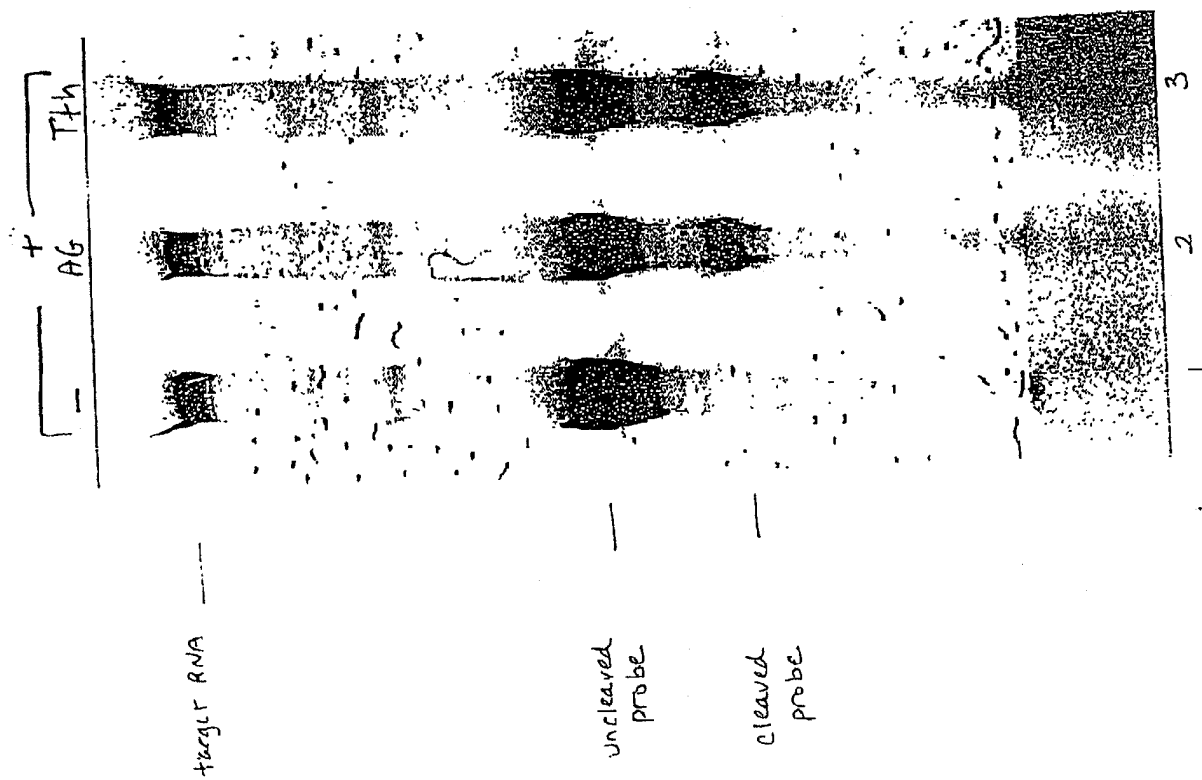
**FIGURE 41**



**FIGURE 42B**



**FIGURE 42A**



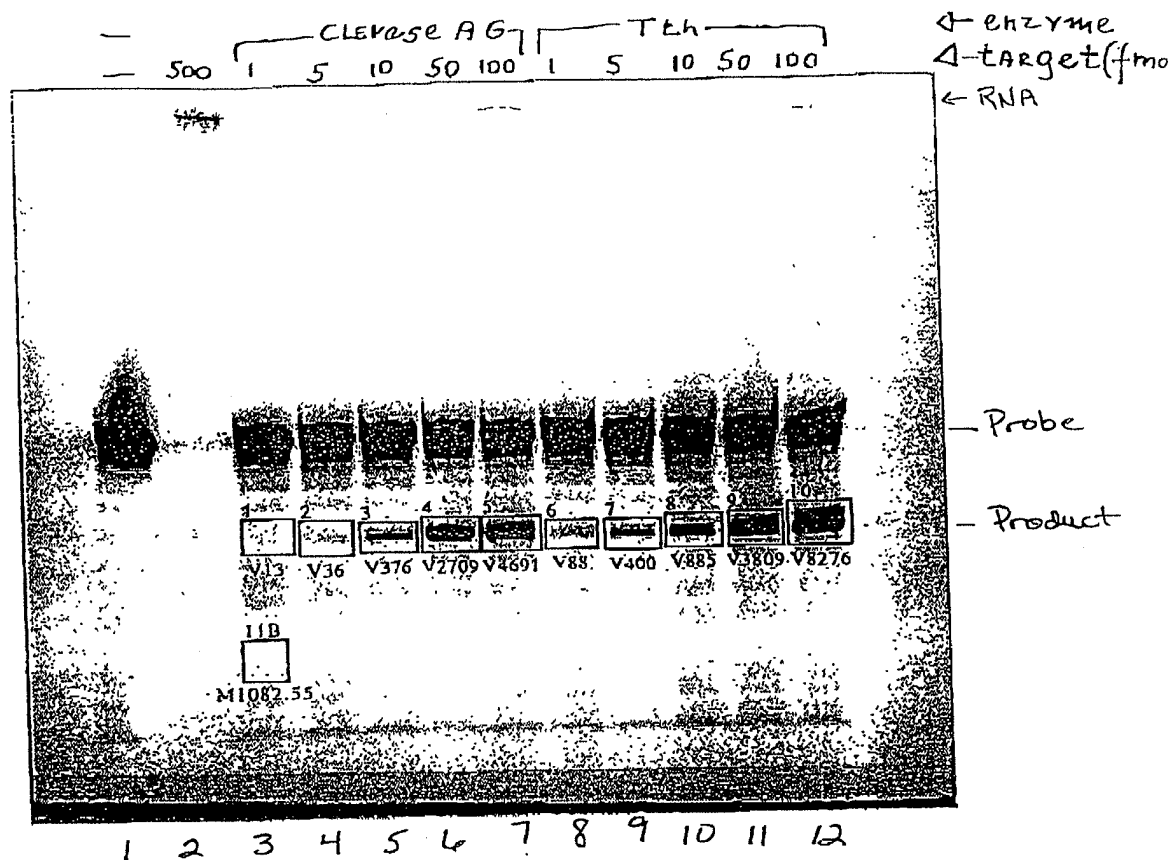
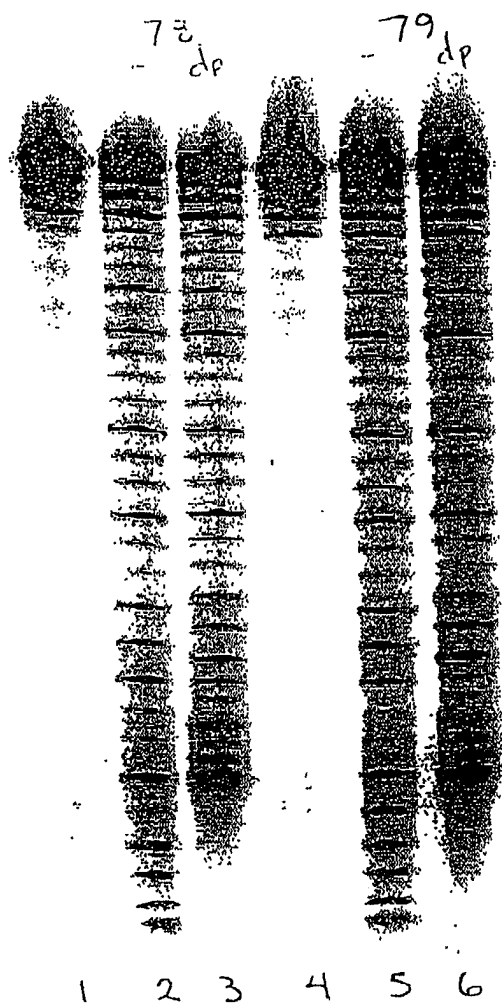


FIGURE 43



**FIGURE 44**



FIGURE 45

70 (C10 aminoT's)

74 (C6 amino T's)

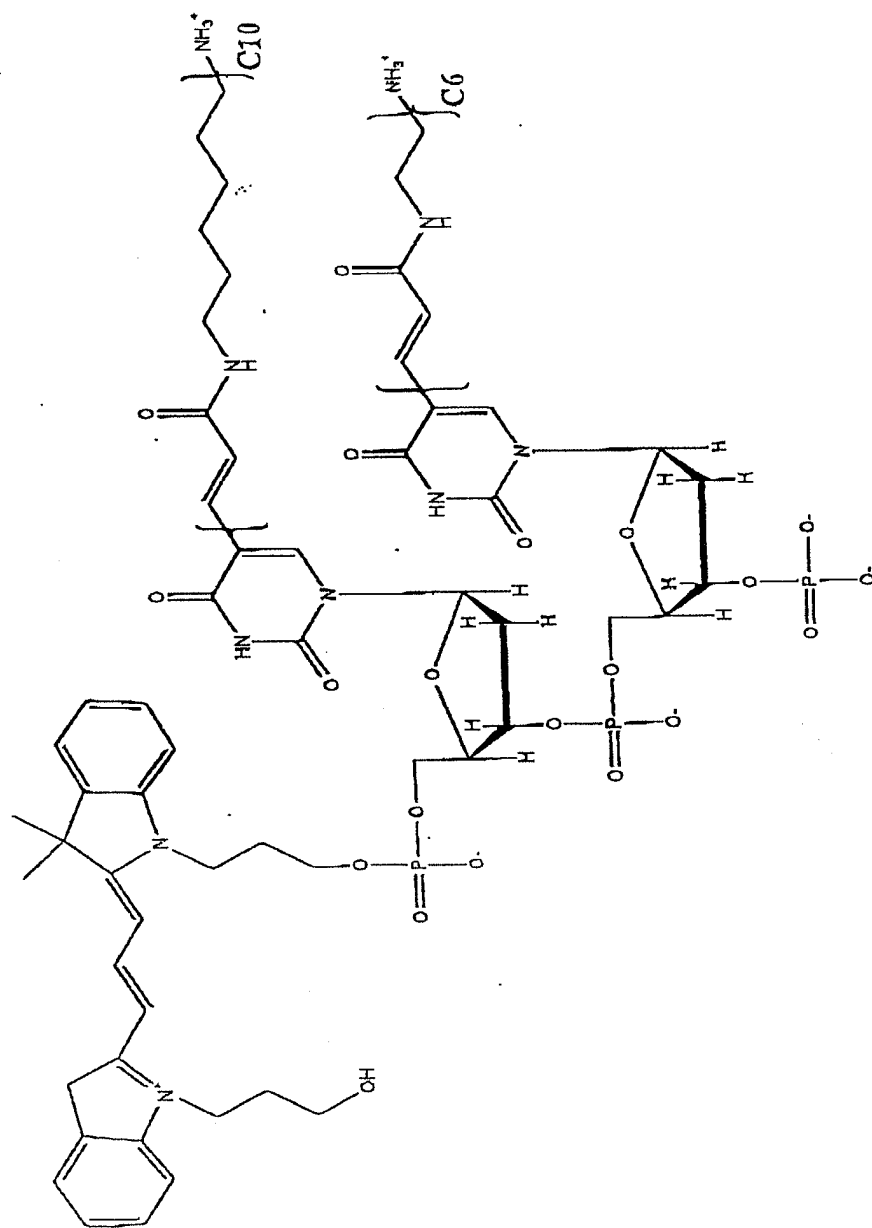


FIGURE 46

75

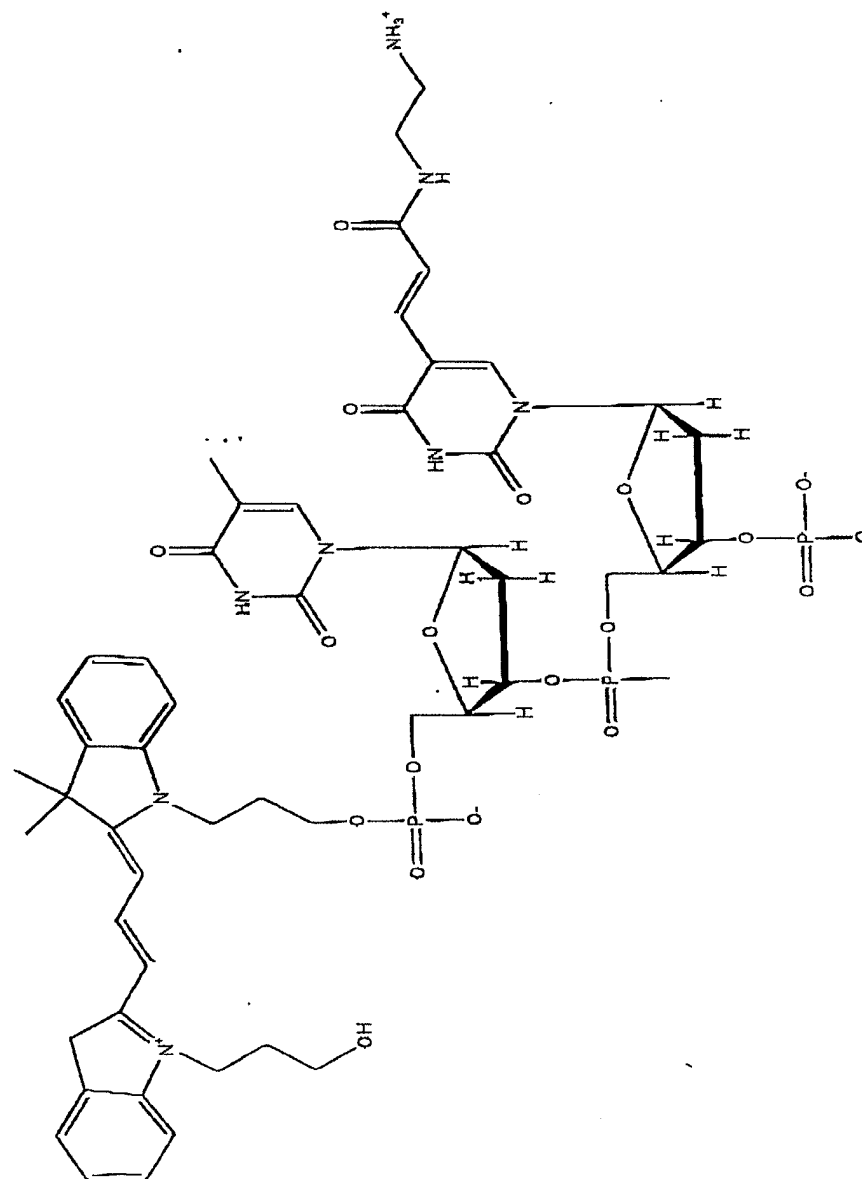
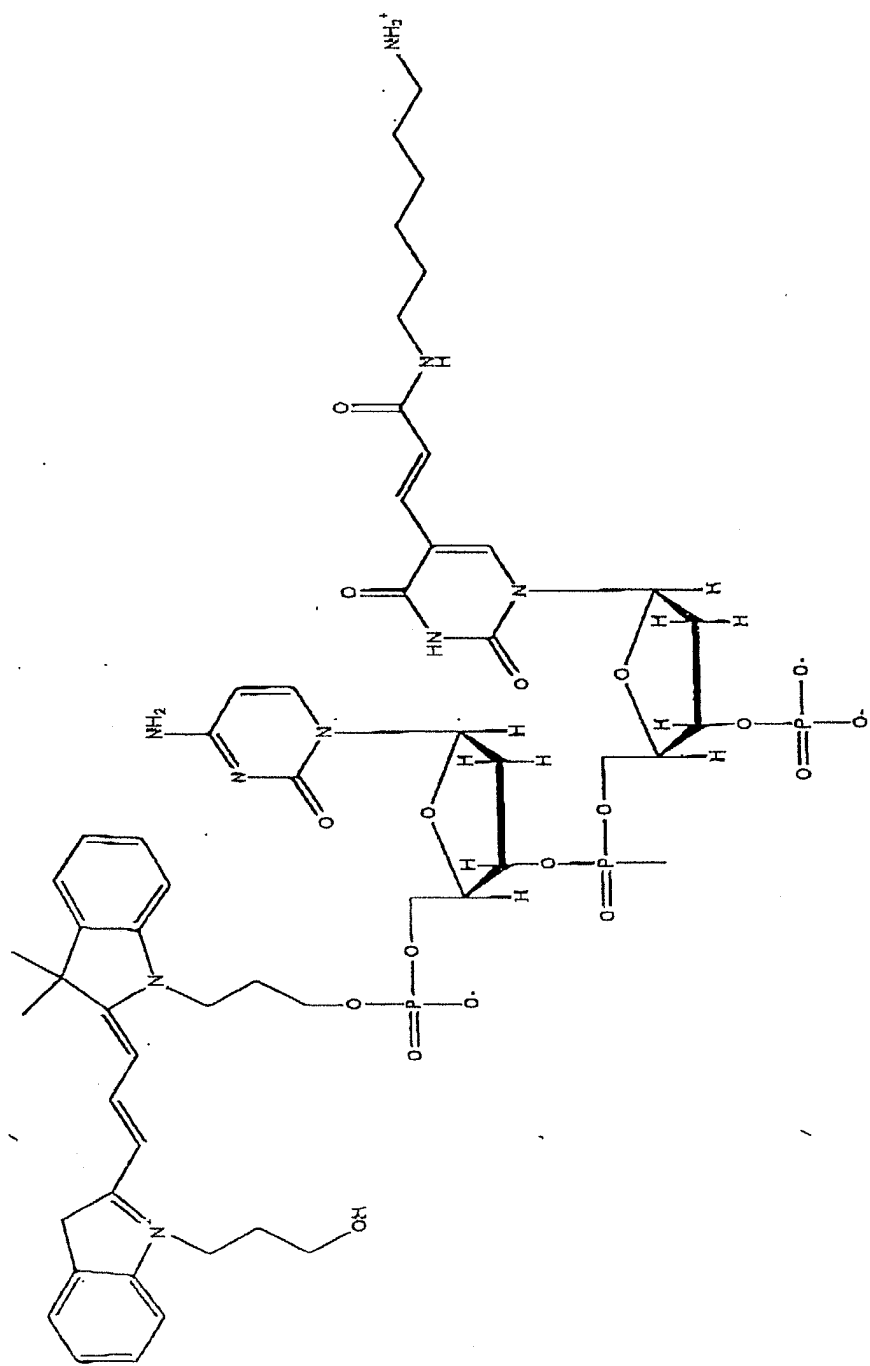
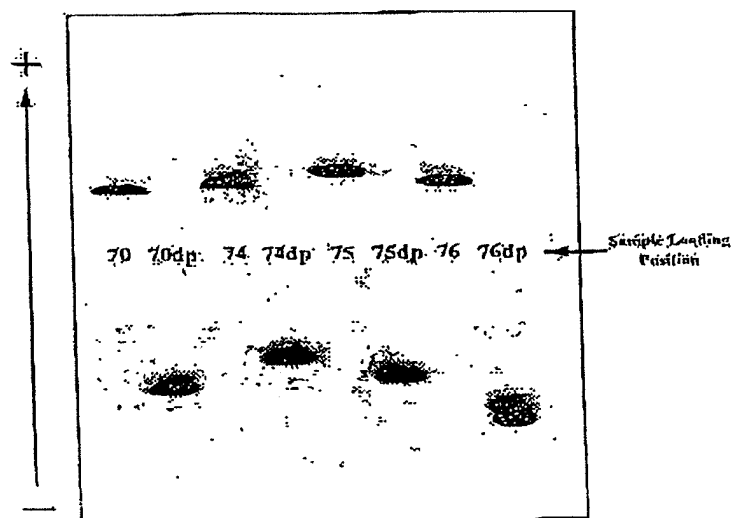


FIGURE 47

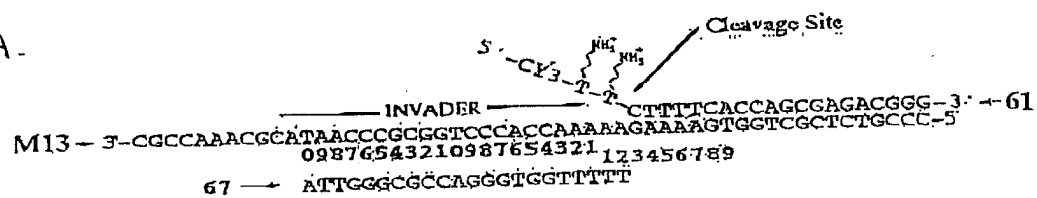
76



**FIGURE 48**



A.



B.

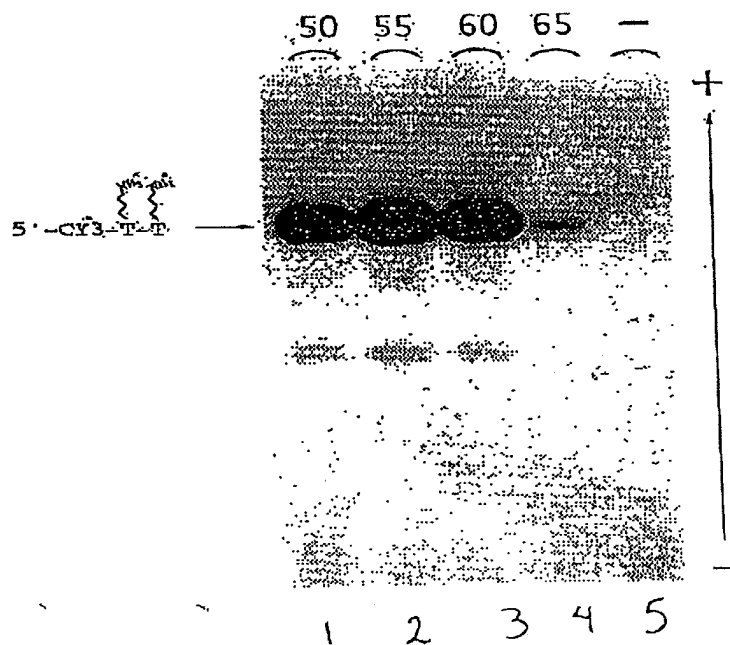


FIGURE 49

FIGURE 50

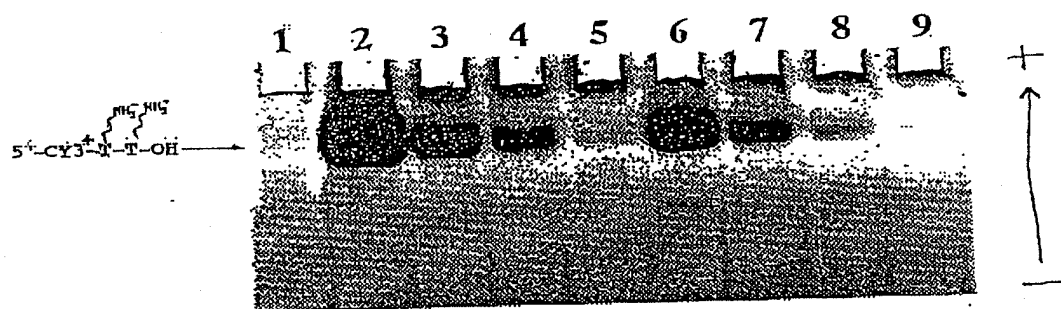


FIGURE 51

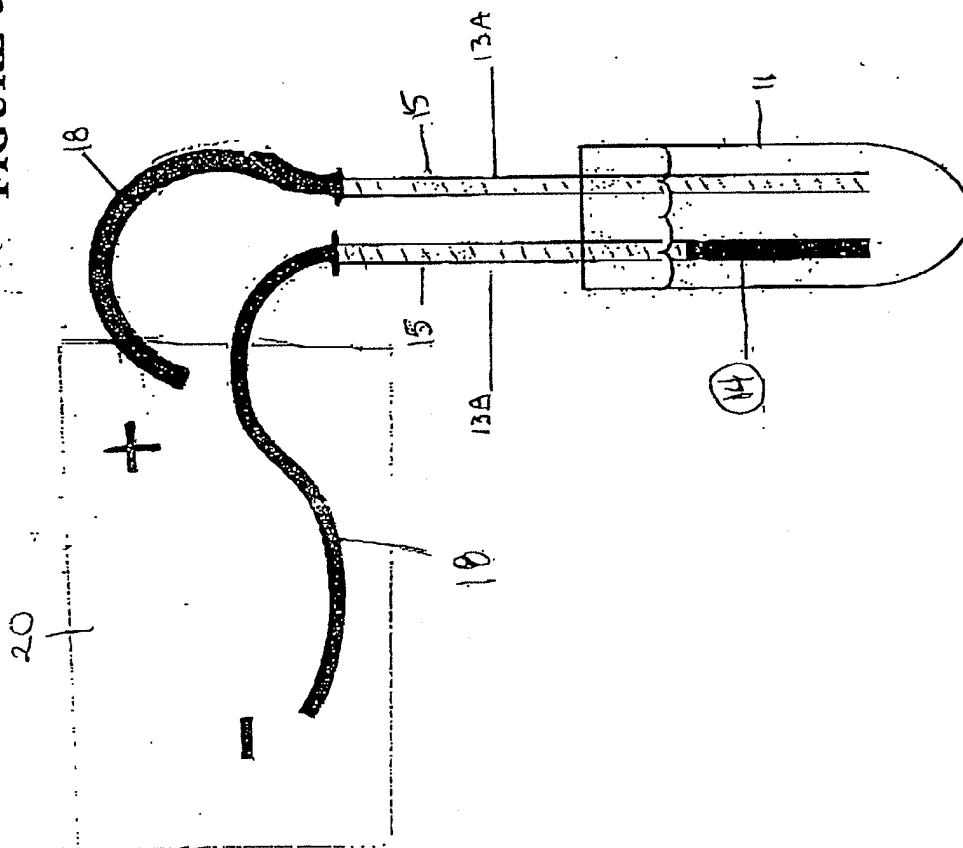
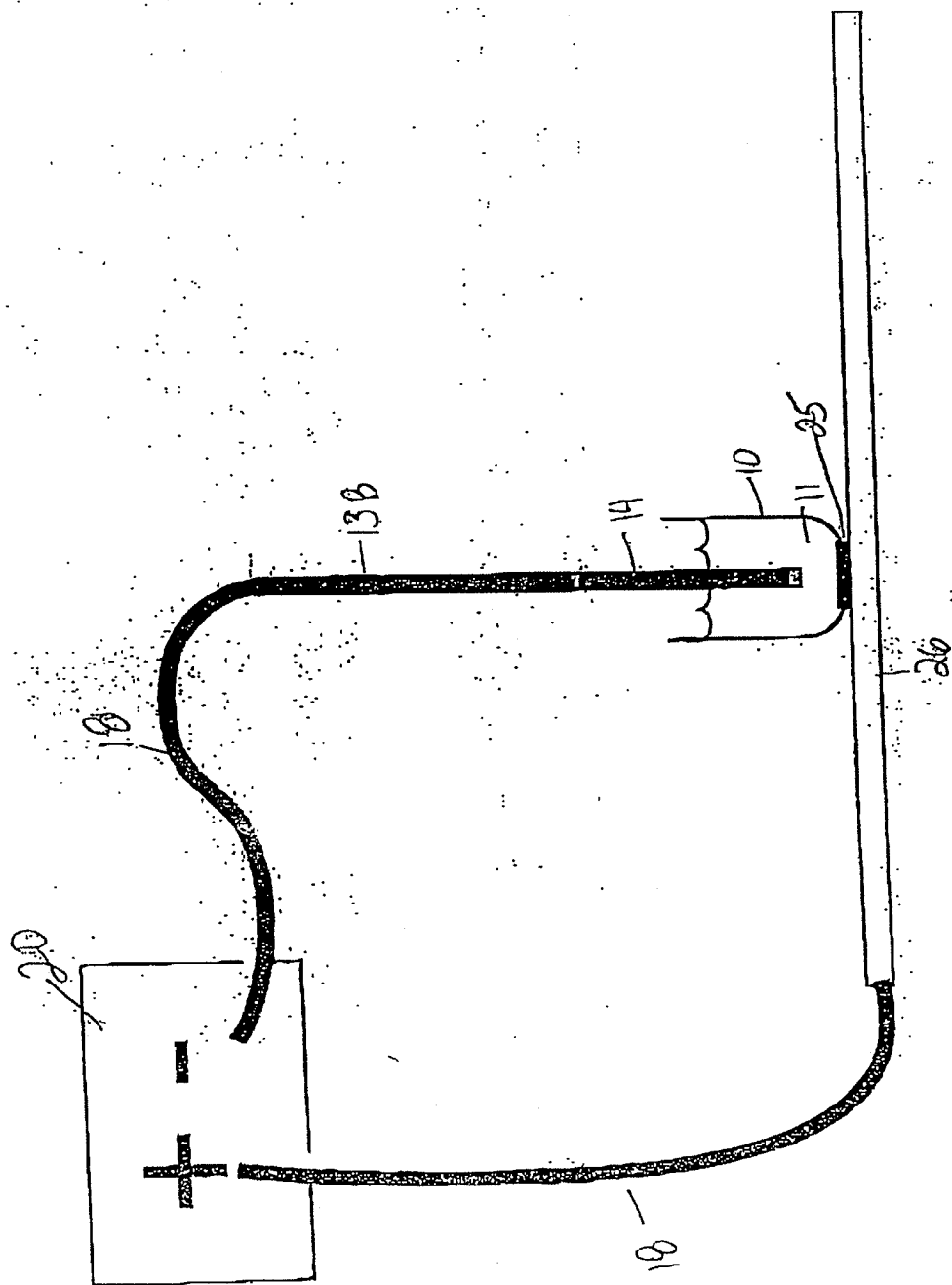
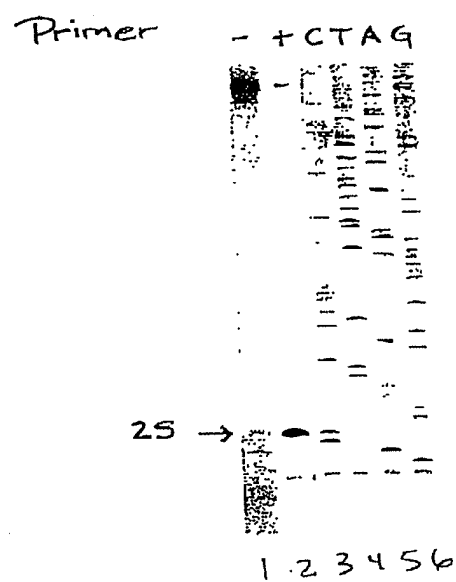


FIGURE 52





**FIGURE 53**



5' AGAAAGGAAGGGAAGAAAGCGAAAGG 3'  
 3' CGGCCGCTTGCACCGCTCTTTCCTTCCCTTCTTTCGCTTTCC 5'

AGAAAGGA  
 5' GCCGGCGAACGTGGCGAGAAAGGAAGGGAAGAAAGCGAAAGG 3'  
 3' CGGCCGCTTGCACCGCTCTTTCCTTCCCTTCTTTCGCTTTCC 5'

a

5' CAG AAGGAAGGGAAGAAAGCGAAAGG 3'  
 3' CGGCCGCTTGCACCGCTCTTTCCTTCCCTTCTTTCGCTTTCC 5'

CAGAAGGA  
 5' GCCGGCGAACGTGGCGAGAAAGGAAGGGAAGAAAGCGAAAGG 3'  
 3' CGGCCGCTTGCACCGCTCTTTCCTTCCCTTCTTTCGCTTTCC 5'

b

5' CAGGG GGAAGGGAAGAAAGCGAAAGG 3'  
 3' CGGCCGCTTGCACCGCTCTTTCCTTCCCTTCTTTCGCTTTCC 5'

CAGGGGA  
 5' GCCGGCGAACGTGGCGAGAAAGGAAGGGAAGAAAGCGAAAGG 3'  
 3' CGGCCGCTTGCACCGCTCTTTCCTTCCCTTCTTTCGCTTTCC 5'

c

5' CAGGGTAC AGGGAAGAAAGCGAAAGG 3'  
 3' CGGCCGCTTGCACCGCTCTTTCCTTCCCTTCTTTCGCTTTCC 5'

CAGGGTAC  
 5' GCCGGCGAACGTGGCGAGAAAGGAAGGGAAGAAAGCGAAAGG 3'  
 3' CGGCCGCTTGCACCGCTCTTTCCTTCCCTTCTTTCGCTTTCC 5'

d

FIGURE 54

**FIGURE 55**

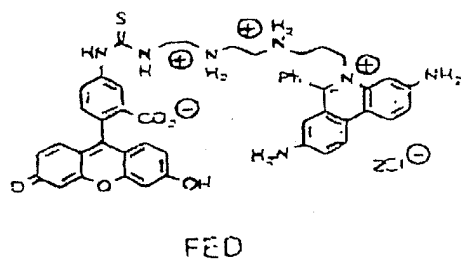
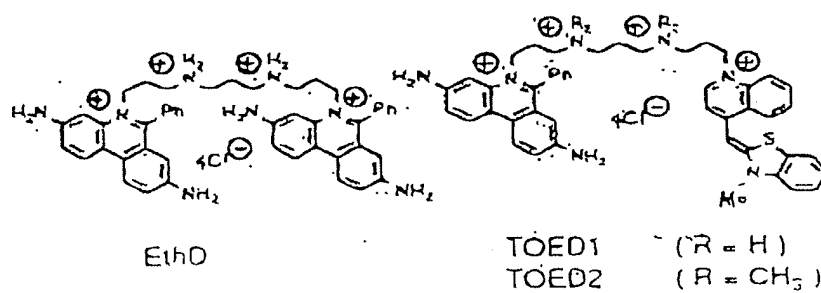
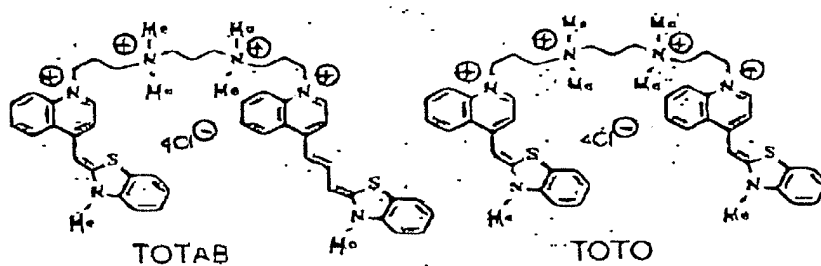
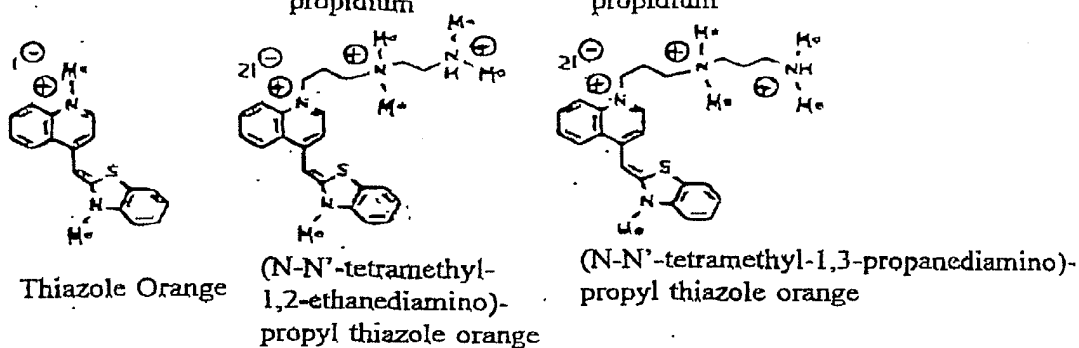
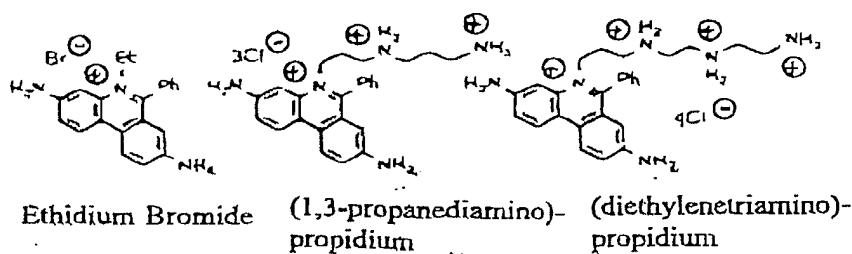


FIGURE 56

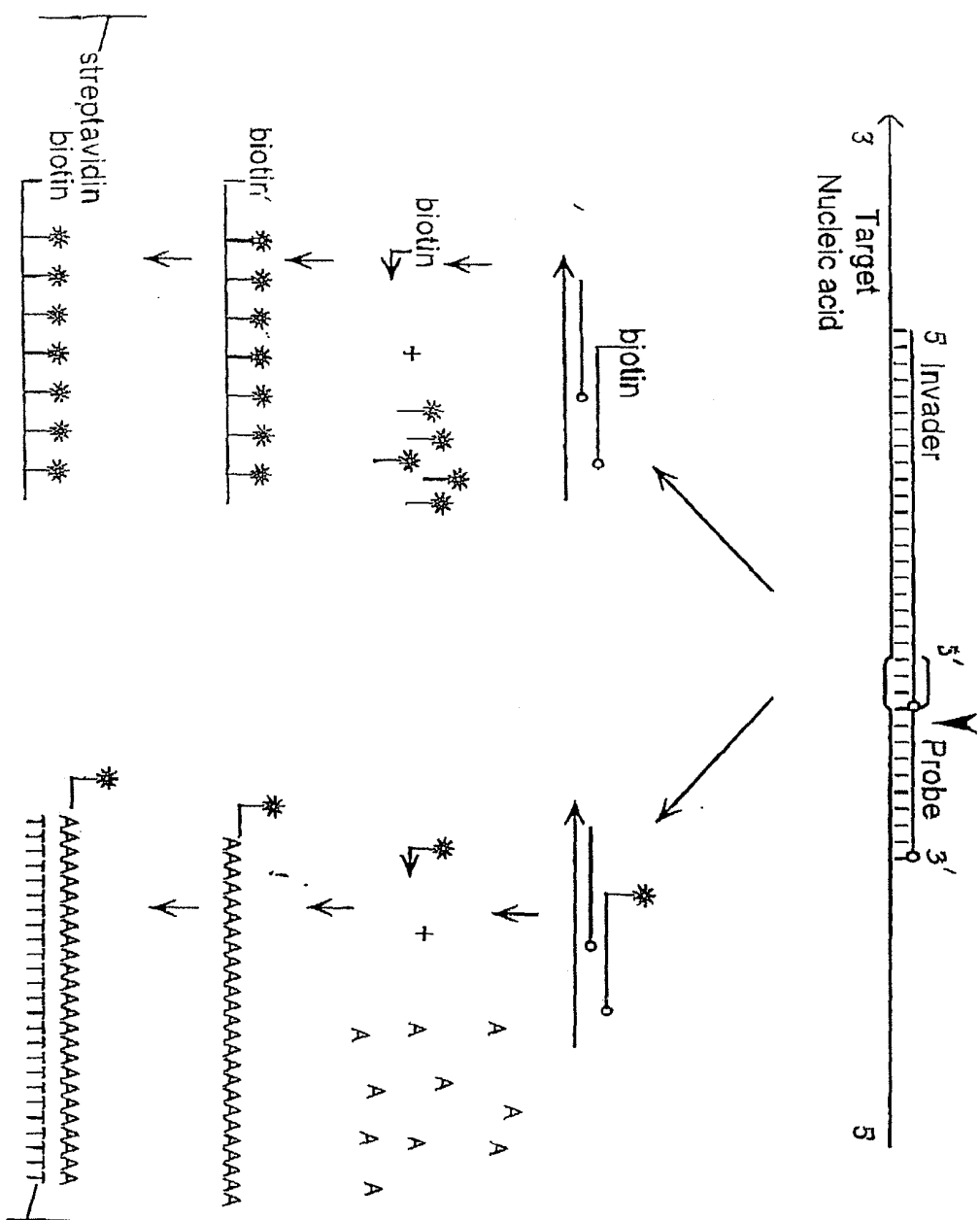
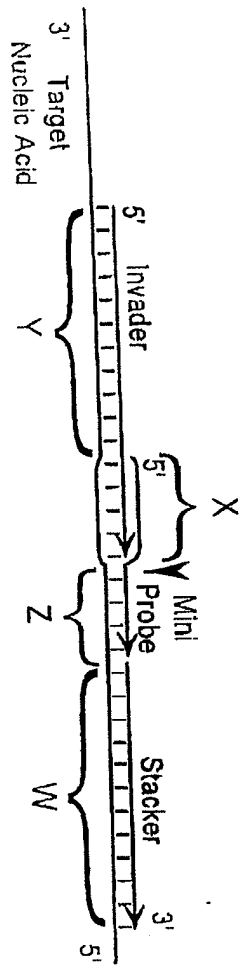


FIGURE 57



**FIGURE 58**



71

[illegible]

72.



FIGURE 59C

	290	300	310	320	330	340	350
1	NEVEYDEIKRIFKEPV	-----	-----	TD--NYSLSKLDPKEGI	IKFLVDENDFN	YD	MJAFEN1.PRO
2	SDVDLTAIKEFFLNPRV	-----	-----	TO--NYNLVWROPEEGIL	KFLCDEHOFSE		PFUFEN1.PRO
3	ENWLEKREAHOLFLEPEV	-----	-----	LOPESVELKWESENEEEL	IKFMCGEKOFSE		HUMFEN1.PRO
4	ENWLEKREAHOLFLEPEV	-----	-----	VOPESVELKWESENEEEL	VKFMCGEKOFSE		MUSFEN1.PRO
5	EDWPKGARMFLLOPEV	-----	-----	IDGNEINLKWSPKKEKEL	IEYLCDDKKFSEE		YST510.PRO
6	ENKFEKDLRKLKLYNNEI	ILDDDFPSVHYDAYMRPEVDH	OTPFVWGVPDLOMLRSFMK	TOLGWPH			YSTRAD2.PRO
7	OVNTPVKKRINKLVGK	-ILPSEFPNPLVDEAYLHP	AVDDSKOSFOWGI	POLOELROFLMATV	WSKO		SPORAD13.PRO
8	ENPNDTKVKKKL	--RTLQLTGFPNPAVAEAYL	KPVDDSKGSFLWGKPD	LOKIREFCORYFGWNR	T		HUMXPG.PRO
9	ENPNDTKVKKKL	--RKLQLTGFPNPAVAEAYL	KPVDDSKGSFLWGKPD	LOKIREFCORYFGWNR	T		MUSXPG.PRO
10	ENPNDTKVKKKL	--RKLQLTGFPNPAVAEAYL	KPVDDSKGSFLWGKPD	LOKIREFCORYFGWNR	T		XENXPG.PRO
11	EKKVSRPHLISTAILLGCDY	FORGVONIGIVSVFO	-ILGEFGDDGNEE	IOPHVILDRFASYVRE			CELRA02.PRO
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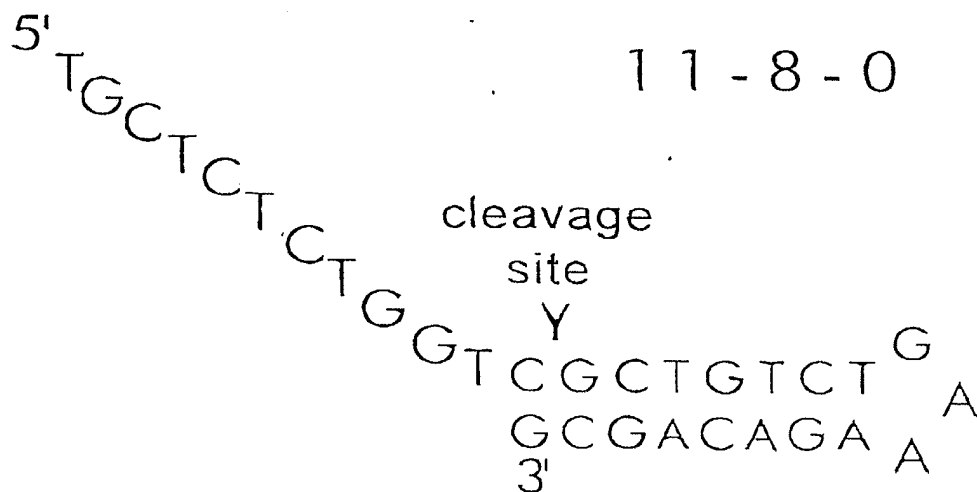
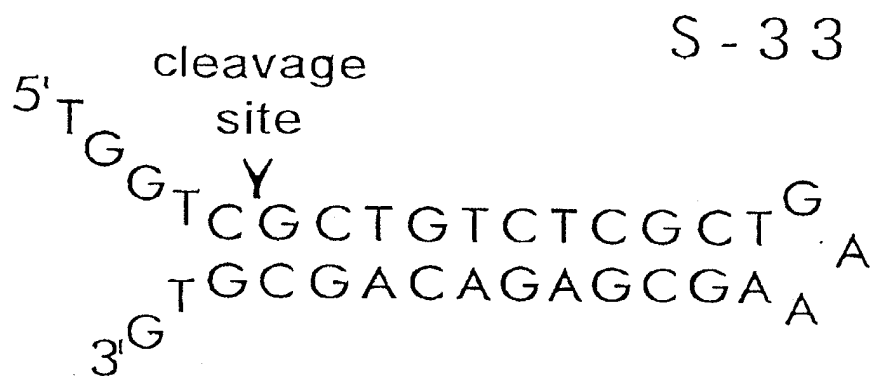
74

[illegible]

FIGURE 59E

1234567891011121314151617181920212223242526272829303132333435363738394041424344454647484950515253545556575859606162636465666768697071727374757677787980818283848586878889909192939495969798991001011021031041051061071081091101111121131141151161171181191201211221231241251261271281291301311321331341351361371381391401411421431441451461471481491501511521531541551561571581591601611621631641651661671681691701711721731741751761771781791801811821831841851861871881891901911921931941951961971981992002012022032042052062072082092102112122132142152162172182192202212222232242252262272282292302312322332342352362372382392402412422432442452462472482492502512522532542552562572582592602612622632642652662672682692702712722732742752762772782792802812822832842852862872882892902912922932942952962972982993003013023033043053063073083093103113123133143153163173183193203213223233243253263273283293303313323333343353363373383393403413423433443453463473483493503513523533543553563573583593603613623633643653663673683693703713723733743753763773783793803813823833843853863873883893903913923933943953963973983994004014024034044054064074084094104114124134144154164174184194204214224234244254264274284294304314324334344354364374384394404414424434444454464474484494504514524534544554564574584594604614624634644654664674684694704714724734744754764774784794804814824834844854864874884894904914924934944954964974984995005015025035045055065075085095105115125135145155165175185195205215225235245255265275285295305315325335345355365375385395405415425435445455465475485495505515525535545555565575585595605615625635645655665675685695705715725735745755765775785795805815825835845855865875885895905915925935945955965975985996006016026036046056066076086096106116126136146156166176186196206216226236246256266276286296306316326336346356366376386396406416426436446456466476486496506516526536546556566576586596606616626636646656666676686696706716726736746756766776786796806816826836846856866876886896906916926936946956966976986997007017027037047057067077087097107117127137147157167177187197207217227237247257267277287297307317327337347357367377387397407417427437447457467477487497507517527537547557567577587597607617627637647657667677687697707717727737747757767777787797807817827837847857867877887897907917927937947957967977987998008018028038048058068078088098108118128138148158168178188198208218228238248258268278288298308318328338348358368378388398408418428438448458468478488498508518528538548558568578588598608618628638648658668678688698708718728738748758768778788798808818828838848858868878888898908918928938948958968978988999009019029039049059069079089099109119129139149159169179189199209219229239249259269279289299309319329339349359369379389399409419429439449459469479489499509519529539549559569579589599609619629639649659669679689699709719729739749759769779789799809819829839849859869879889899909919929939949959969979989991000100110021003100410051006100710081009101010111012101310141015101610171018101910201021102210231024102510261027102810291030103110321033103410351036103710381039104010411042104310441045104610471048104910501051105210531054105510561057105810591060106110621063106410651066106710681069107010711072107310741075107610771078107910801081108210831084108510861087108810891090109110921093109410951096109710981099110011011102110311041105110611071108110911101111111211131114111511161117111811191120112111221123112411251126112711281129113011311132113311341135113611371138113911401141114211431144114511461147114811491150115111521153115411551156115711581159116011611162116311641165116611671168116911701171117211731174117511761177117811791180118111821183118411851186118711881189119011911192119311941195119611971198119912001201120212031204120512061207120812091210121112121213121412151216121712181219122012211222122312241225122612271228122912301231123212331234123512361237123812391240124112421243124412451246124712481249125012511252125312541255125612571258125912601261126212631264126512661267126812691270127112721273127412751276127712781279128012811282128312841285128612871288128912901291129212931294129512961297129812991300130113021303130413051306130713081309131013111312131313141315131613171318131913201321132213231324132513261327132813291330133113321333133413351336133713381339134013411342134313441345134613471348134913501351135213531354135513561357135813591360136113621363136413651366136713681369137013711372137313741375137613771378137913801381138213831384138513861387138813891390139113921393139413951396139713981399140014011402140314041405140614071408140914101411141214131414141514161417141814191420142114221423142414251426142714281429143014311432143314341435143614371438143914401441144214431444144514461447144814491450145114521453145414551456145714581459146014611462146314641465146614671468146914701471147214731474147514761477147814791480148114821483148414851486148714881489149014911492149314941495149614971498149915001501150215031504150515061507150815091510151115121513151415151516151715181519152015211522152315241525152615271528152915301531153215331534153515361537153815391540154115421543154415451546154715481549155015511552155315541555155615571558155915601561156215631564156515661567156815691570157115721573157415751576157715781579158015811582158315841585158615871588158915901591159215931594159515961597159815991600160116021603160416051606160716081609161016111612161316141615161616171618161916201621162216231624162516261627162816291630163116321633163416351636163716381639164016411642164316441645164616471648164916501651165216531654165516561657165816591660166116621663166416651666166716681669167016711672167316741675167616771678167916801681168216831684168516861687168816891690169116921693169416951696169716981699170017011702170317041705170617071708170917101711171217131714171517161717171817191720172117221723172417251726172717281729173017311732173317341735173617371738173917401741174217431744174517461747174817491750175117521753175417551756175717581759176017611762176317641765176617671768176917701771177217731774177517761777177817791780178117821783178417851786178717881789179017911792179317941795179617971798179918001801180218031804180518061807180818091810181118121813181418151816181718181819182018211822182318241825182618271828182918301831183218331834183518361837183818391840184118421843184418451846184718481849185018511852185318541855185618571858185918601861186218631864186518661867186818691870187118721873187418751876187718781879188018811882188318841885188618871888188918901891189218931894189518961897189818991900190119021903190419051906190719081909191019111912191319141915191619171918191919201921192219231924192519261927192819291930193119321933193419351936193719381939194019411942194319441945194619471948194919501951195219531954195519561957195819591960196119621963196419651966196719681969197019711972197319741975197619771978197919801981198219831984198519861987198819891990199119921993199419951996199719981999200020012002200320042005200620072008200920102011201220132014201520162017201820192020202120222023202420252026202720282029203020312032203320342035203620372038203920402041204220432044204520462047204820492050205120522053205420552056205720582059206020612062206320642065206620672068206920702071207220732074207520762077207820792080208120822083208420852086208720882089209020912092209320942095209620972098209921002101210221032104210521062107210821092110211121122113211421152116211721182119212021212122212321242125212621272128212921302131213221332134213521362137213821392140214121422143214421452146214721482149215021512152215321542155215621572158215921602161216221632164216521662167216821692170217121722173217421752176217721782179218021812182218321842185218621872188218921902191219221932194219521962197219821992200220122022203220422052206220722082209221022112212221322142215221622172218221922202221222222232224222522262227222822292230223122322233223422352236223722382239224022412242224322442245224622472248224922502251225222532254225522562257225822592260226122622263226422652266226722682269227022712272227322742275227622772278227922802281228222832284228522862287228822892290229122922293229422952296229722982299230023012302230323042305230623072308230923102311231223132314231523162317231823192320232123222323232423252326232723282329233023312332233323342335233623372338233923402341234223432344234523462347234823492350235123522353235423552356235723582359236023612362236323642365236623672368236923702371237223732374237523762377237823792380238123822383238423852386238723882389239023912392239323942395239623972398239924002401240224032404240524062407240824092410241124122413241424152416241724182419242024212422242324242425242624272428242924302431243224332434243524362437243824392440244124422443244424452446244724482449245024512452245324542455245624572458245924602461246224632464246524662467246824692470247124722473247424752476247724782479248024812482248324842485248624872488248924902491249224932494249524962497249824992500250125022503250425052506250725082509251025112512251325142515251625172518251925202521252225232524252525262527252825292530253125322533253425352536253725382539254025412542254325442545254625472548254925502551255225532554255525562557255825592560256125622563256425652566256725682569257025712572257325742575257625772578257925802581258225832584258525862587258825892590259125922593259425952596259725982599260026012602260326042605260626072608260926102611261226132614261526162617261826192620262126222623262426252626262726282629263026312632263326342635263626372638263926402641264226432644264526462647264826492650265126522653265426552656265726582659266026612662266326642665266626672668266926702671267226732674267526762677267826792680268126822683268426852686268726882689269026912692269326942695269626972698269927002701270227032704270527062707270827092710271127122713271427152716271727182719272027212722272327242725272627272728272927302731273227332734273527362737273827392740274127422743274427452746274727482749275027512752275327542755275627572758275927602761276227632764276527662767276827692770277127722773277427752776277727782779278027812782278327842785278627872788278927902791279227932794279527962797279827992800280128022803280428052806280728082809281028112812281328142815281628172818281928202821282228232824282528262827282828292830283128322833283428352836283728382839284028412842284328442845284628472848284928502851285228532854285528562857285828592860286128622863286428652866286728682869287028712872287328742875287628772878287928802881288228832884288528862887288828892890289128922893289428952896289728982899290029012902290329042905290629072908290929102911291229132914291529162917291829192920292129222923292429252926292729282929293029312932293329342935293629372938293929402941294229432944294529462947294829492950295129522953295429552956295729582959296029612962296329642965296629672968296929702971297229732974297529762977297829792980298129822983298429852986298729882989299029912992299329942995299629972998299930003001300230033004300530063007300830093010301130123013301430153016301730183019302030213022302330243025302630273028302930303031303230333034303530363037303830393040304130423043304430453046304730483049305030513052305330543055305630573058305930603061306230633064306530663067306830693070307130723073307430753076307730783079308030813082308330843085308630873088308930903091309230933094309530963097309830993100310131023103310431053106310731083109311031113112311331143115311631173118311931203121312231233124312531263127312831293130313131323133313431353136313731383139314031413142314331443145314631473148314931503151315231533154315531563157315831593160316131623163316431653166316731683169317031713172317331743175317631773178317931803181318231833184318531863187318831893190319131923193319431953196319731983199320032013202320332043205320632073208320932103211321232133214321532163217321832193220322132223223322343225322632273228322932303231323232333234323532363237323832393240324132423243324432453246324732483249325032513252325332543255325632573258325932603261326232633264326532663267326832693270327132723273327432753276327732783279328032813282328332843285328632873288328932903291329232933294329532963297329832993300330133023303330433053306330733083309331033113312331333143315331633173318331933203321332233233324332533263327332833293330333133323333333433353336333733383339334033413342334333443345334633

FIGURE 60



**FIGURE 61**

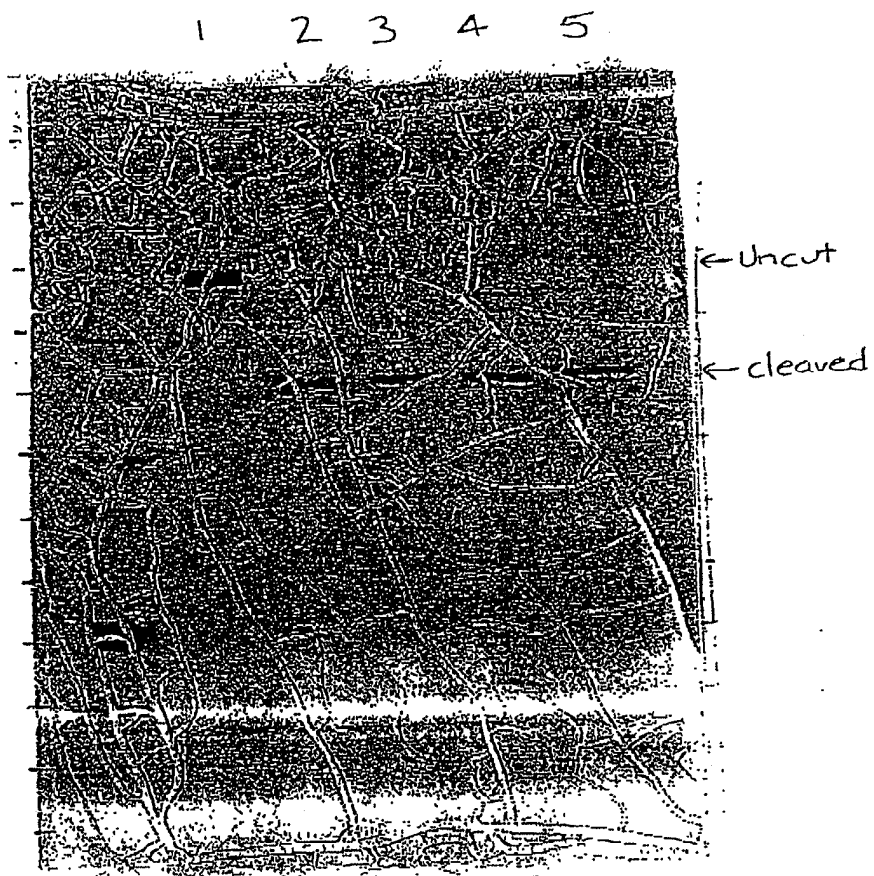
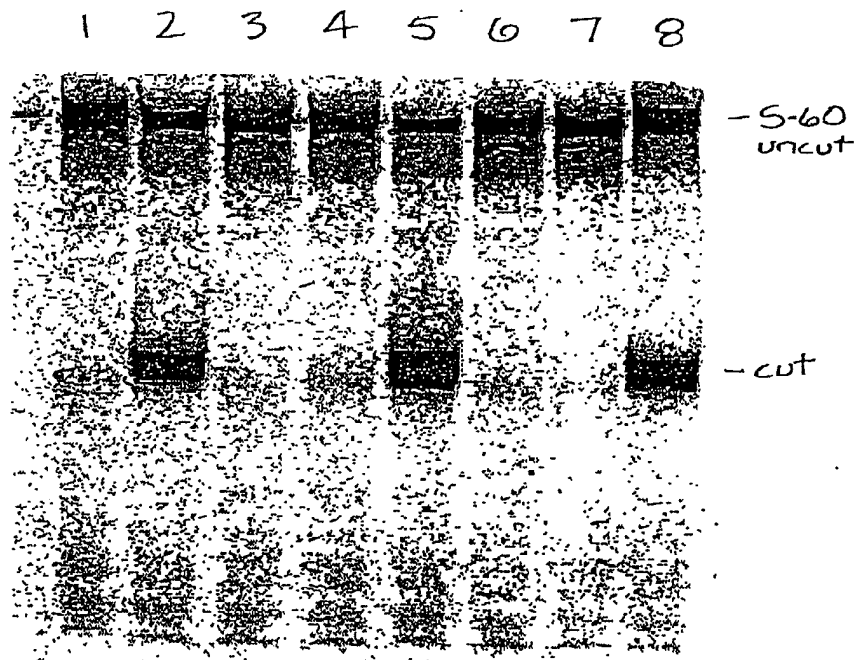
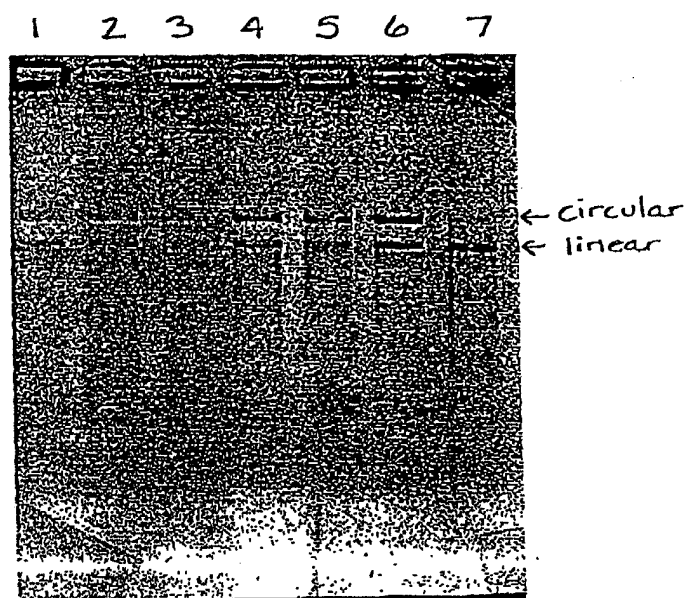
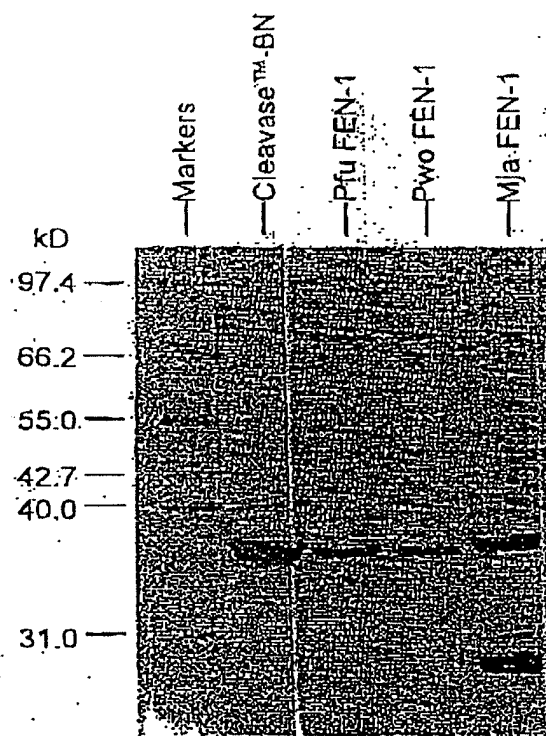


FIGURE 62



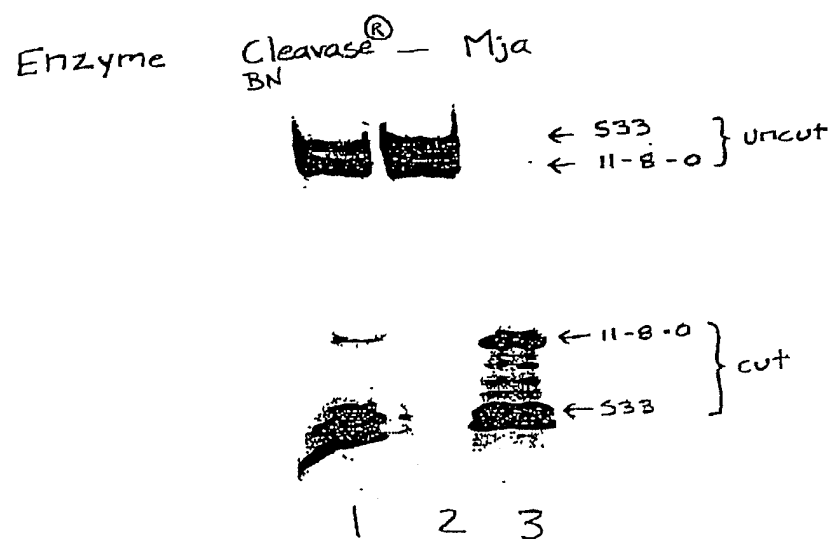
**FIGURE 63**



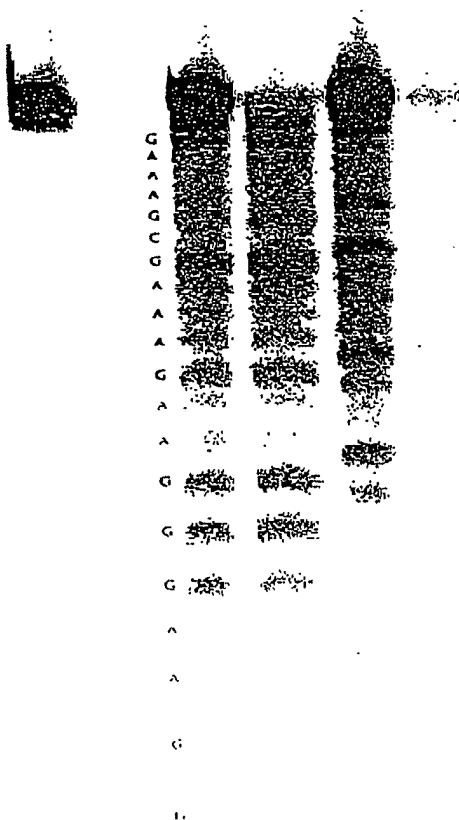


**FIGURE 64**





**FIGURE 65**



5'-nAGAAggaaggga agaaagcgaaagG-3'

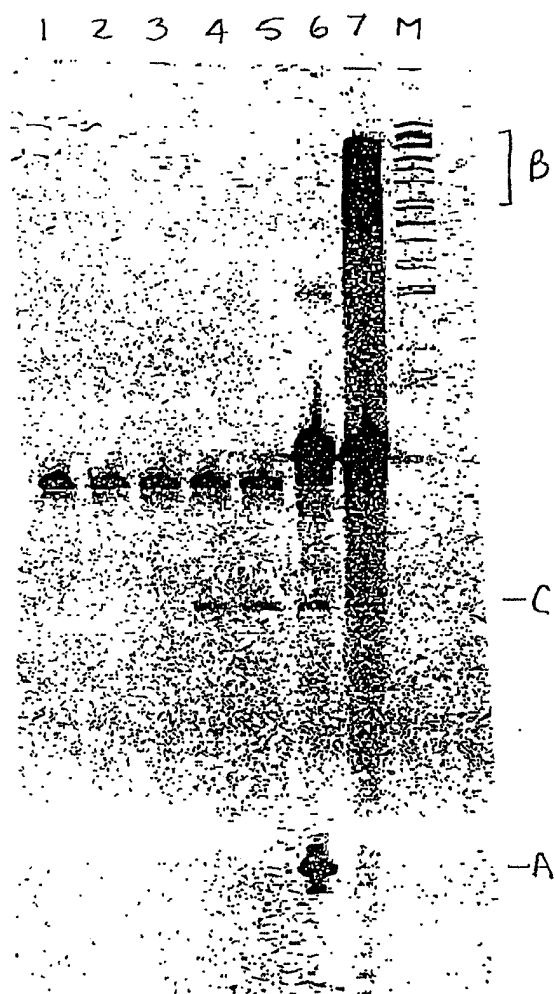


FIGURE 67

FIGURE 68

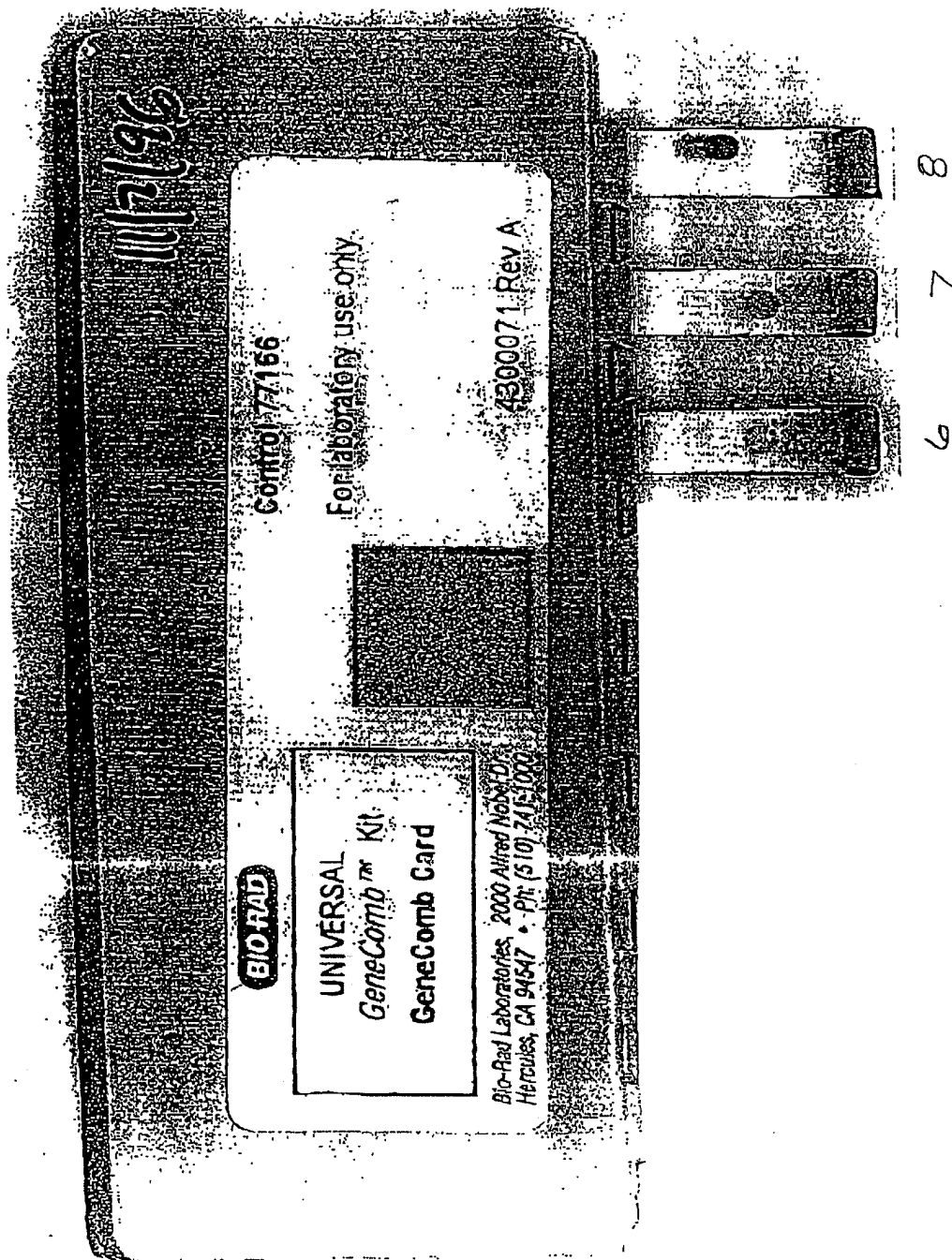


FIGURE 69

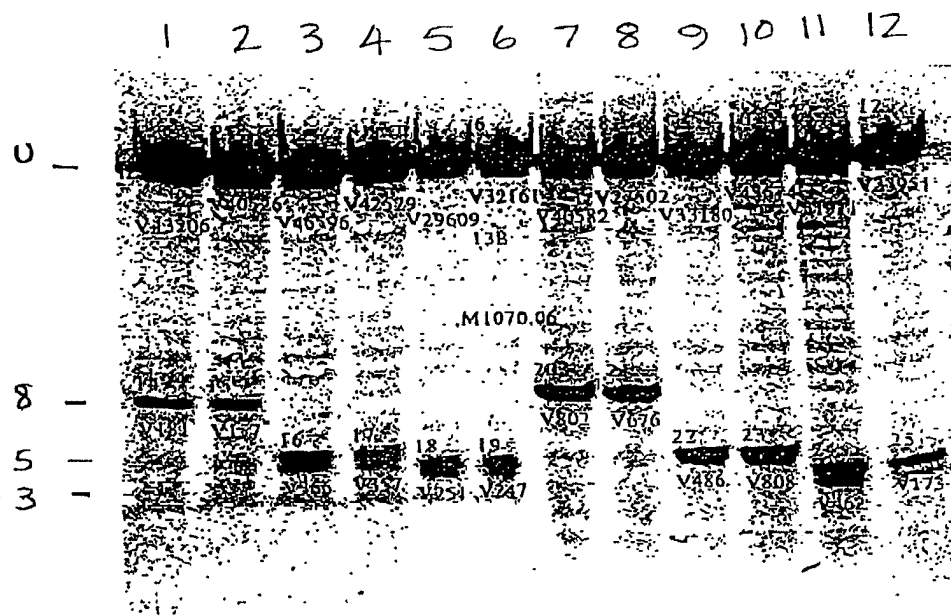
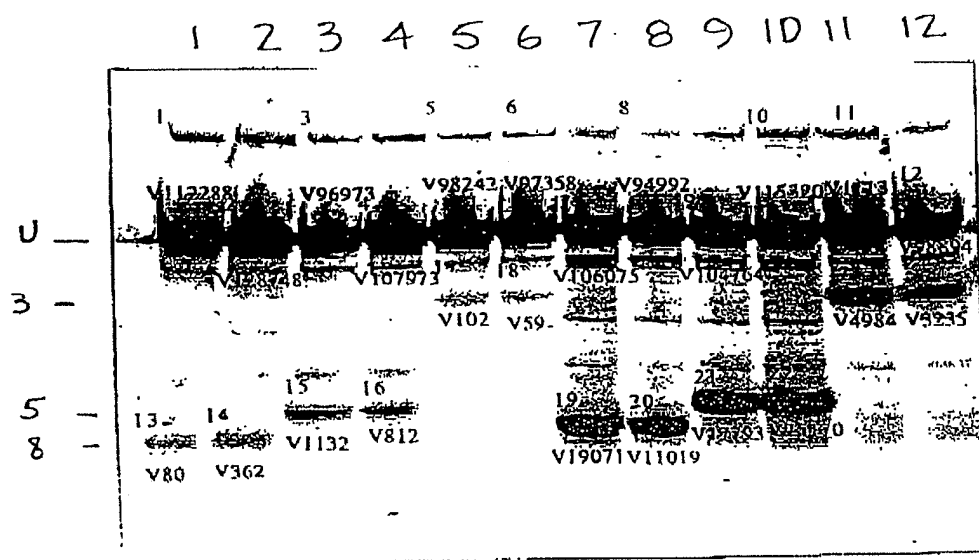
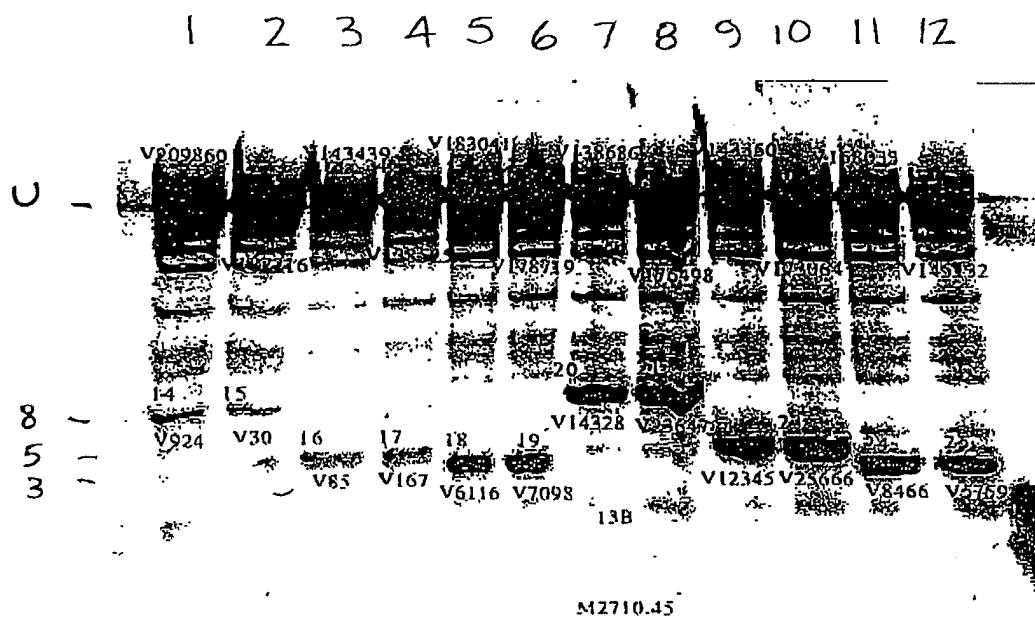


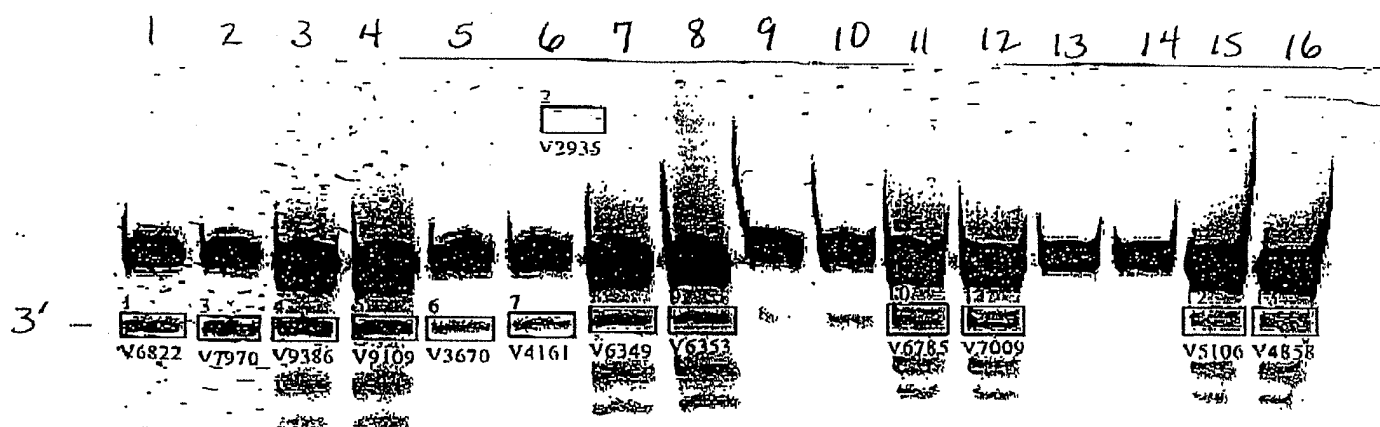
FIGURE 70



### FIGURE 71



A



B

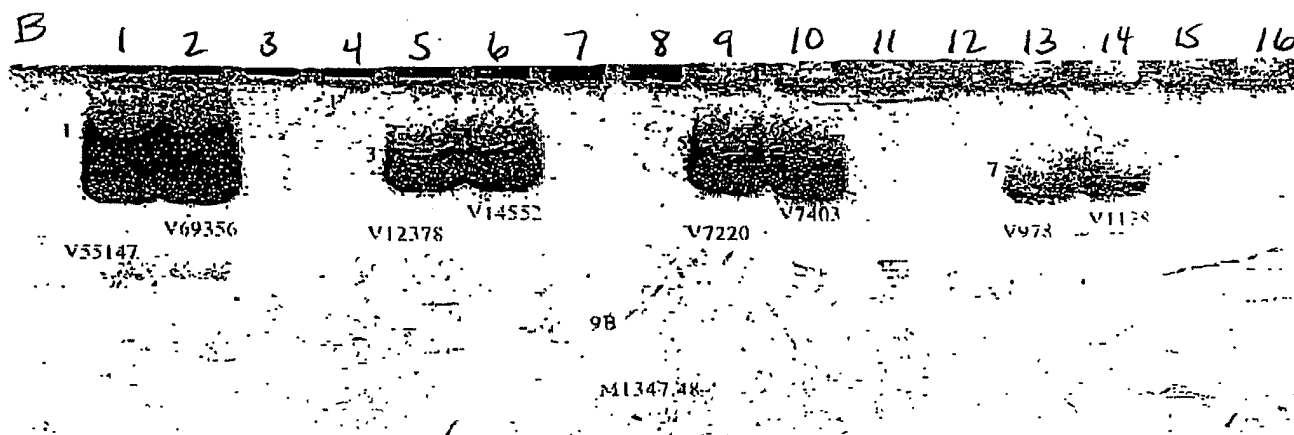
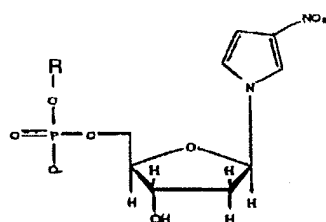


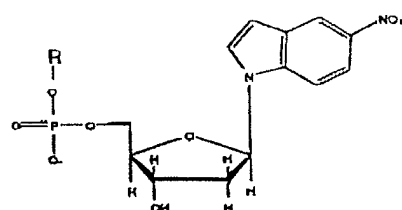
FIGURE 72



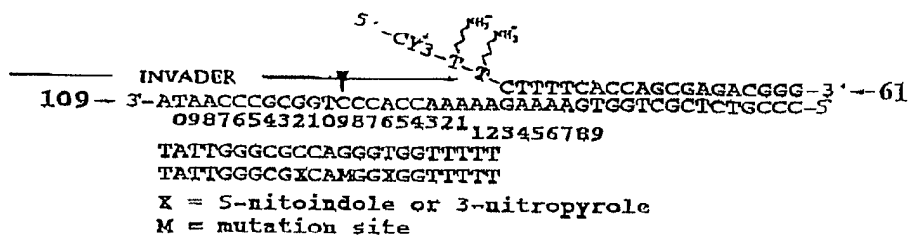
**FIGURE 73**



**3-nitropyrrole**



**5-nitroindole**

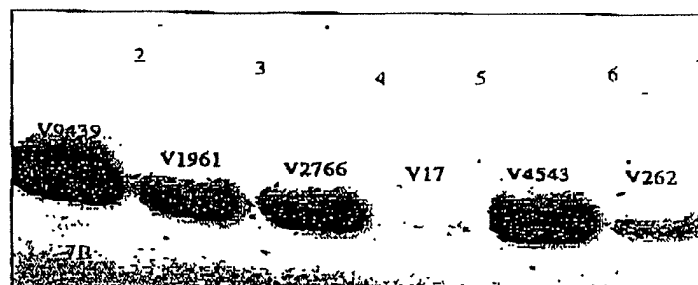


**FIGURE 74**

	Allcomp	1Base Mismatch	Allcomp	1Base Mismatch	Allcomp	1Base Mismatch
	2NI	2NI	1NP	1NP	1NP	1NP
Inuall #	67	114	115	116	112	113

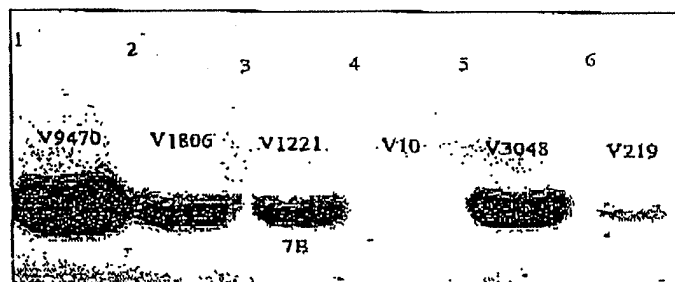
A

52°C



B

55°C



C

58°C

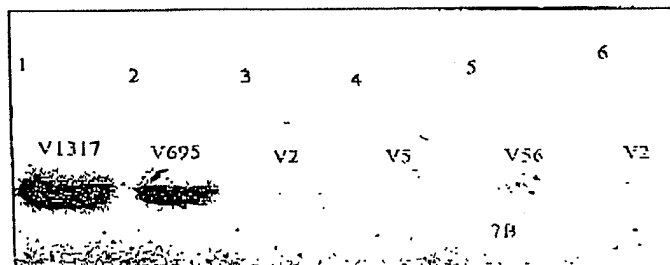
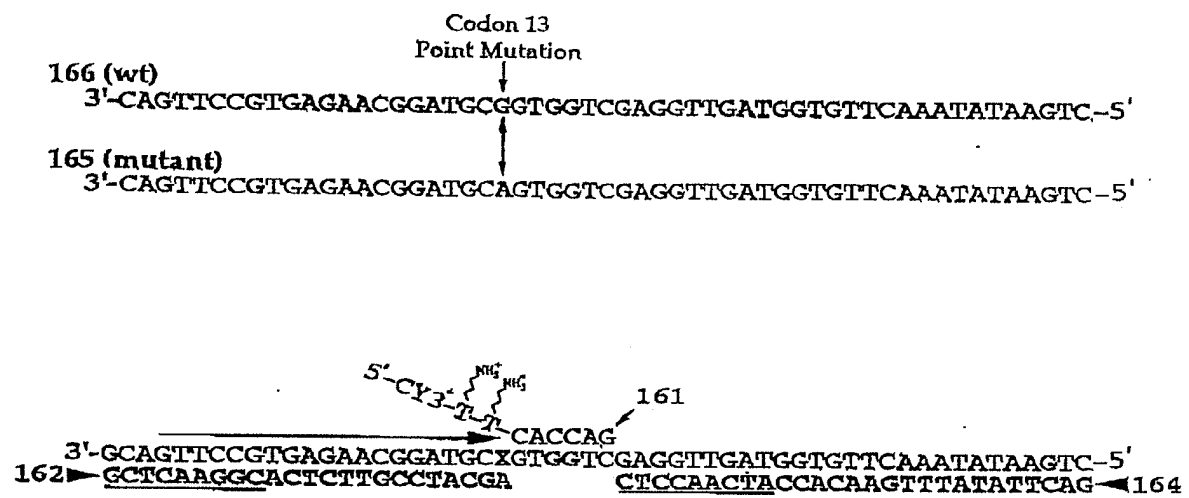
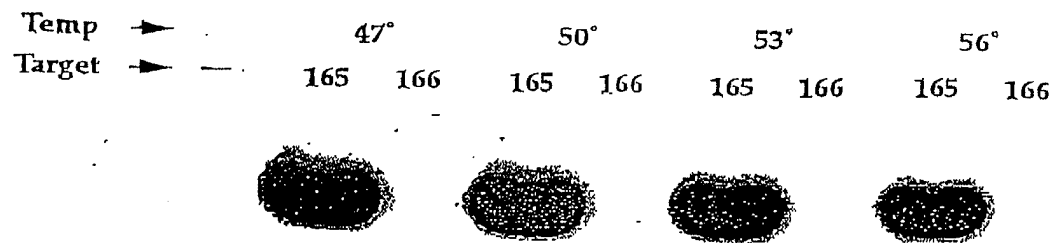


FIGURE 75

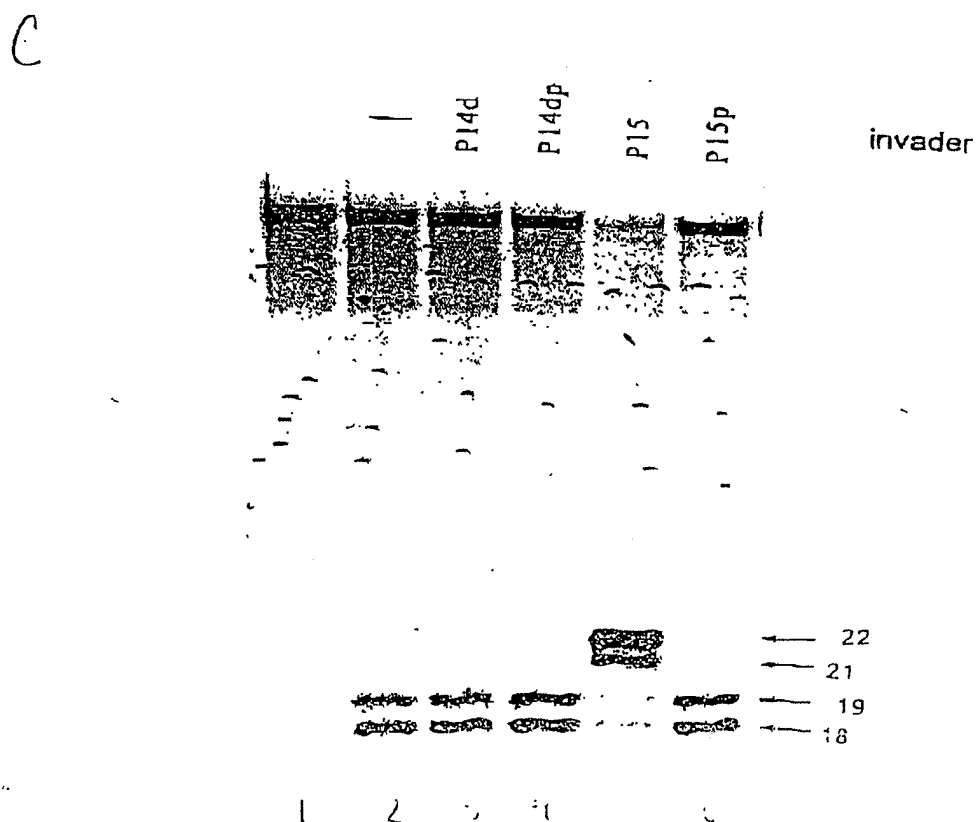
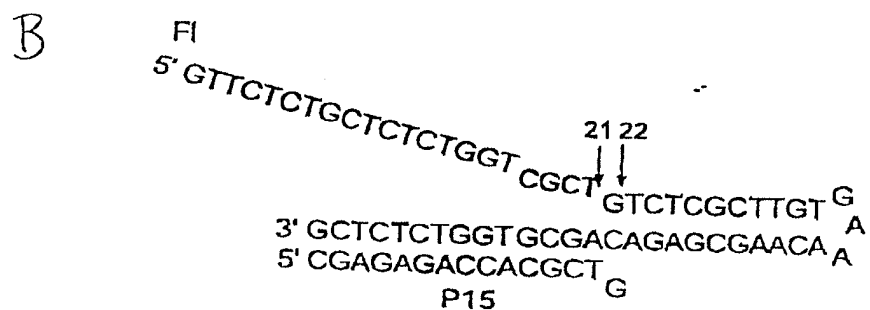
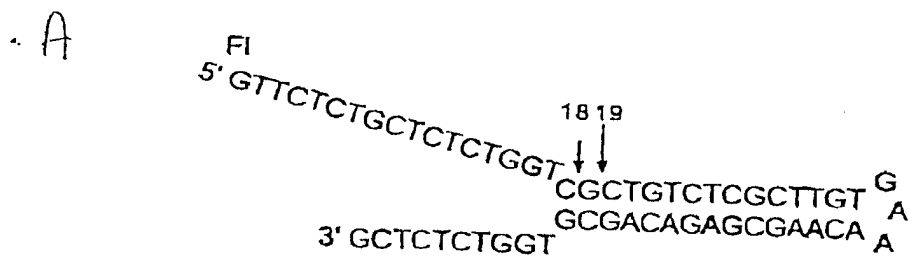
**FIGURE 76**



**FIGURE 77**



**FIGURE 78**



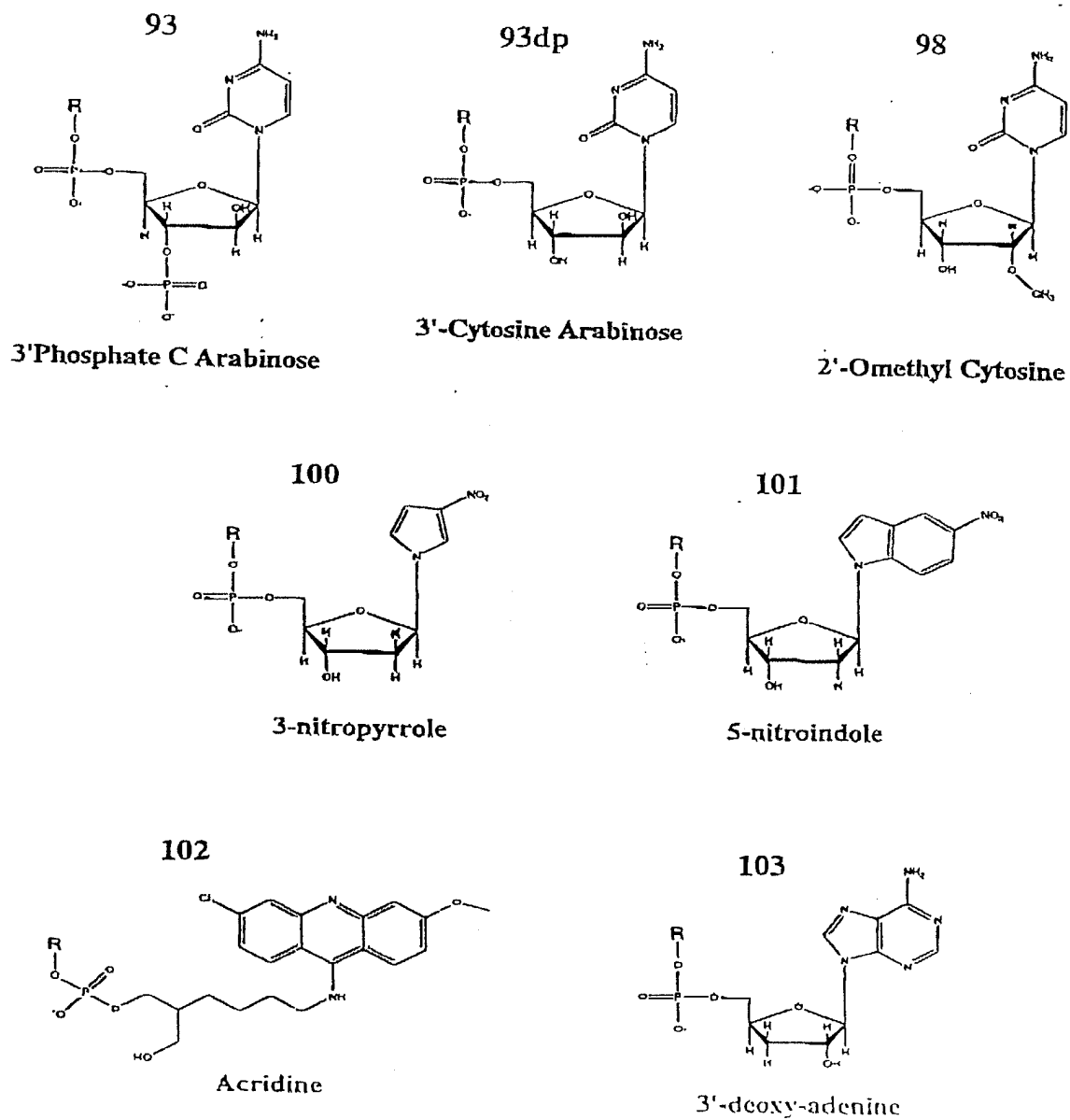


FIGURE 79

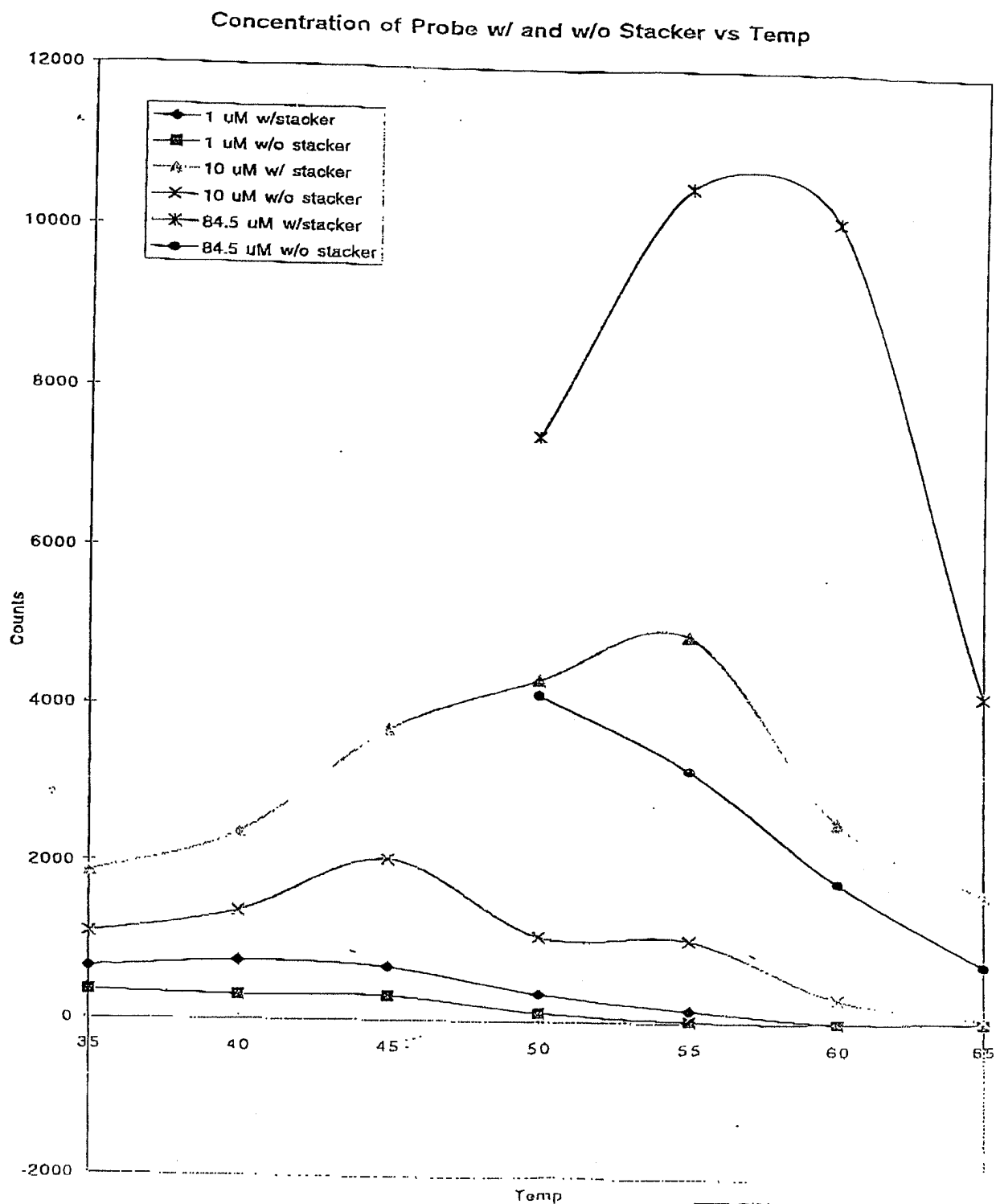
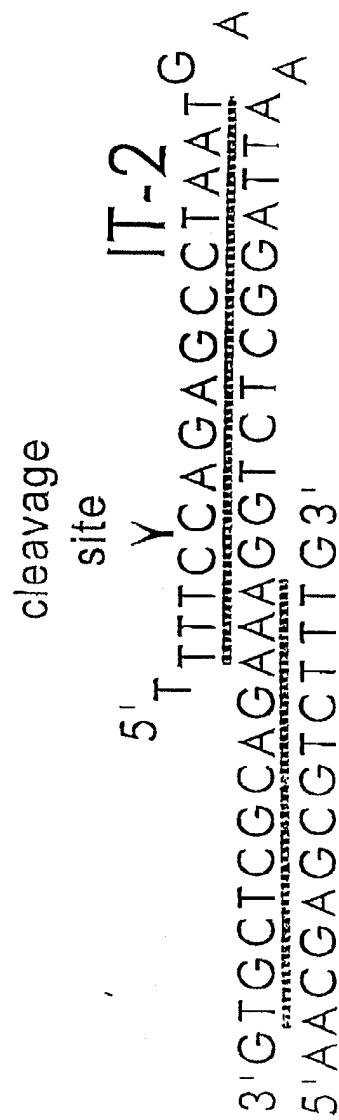


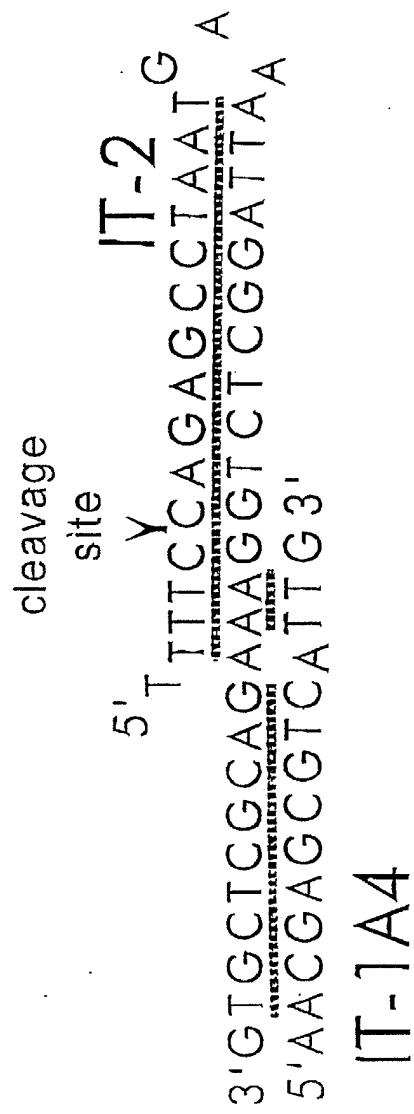
FIGURE 80



FIGURE 81

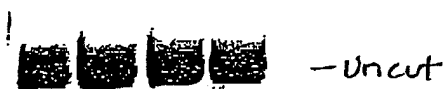


IT-1



# FIGURE 82

1 2 3 4



**FIGURE 83**

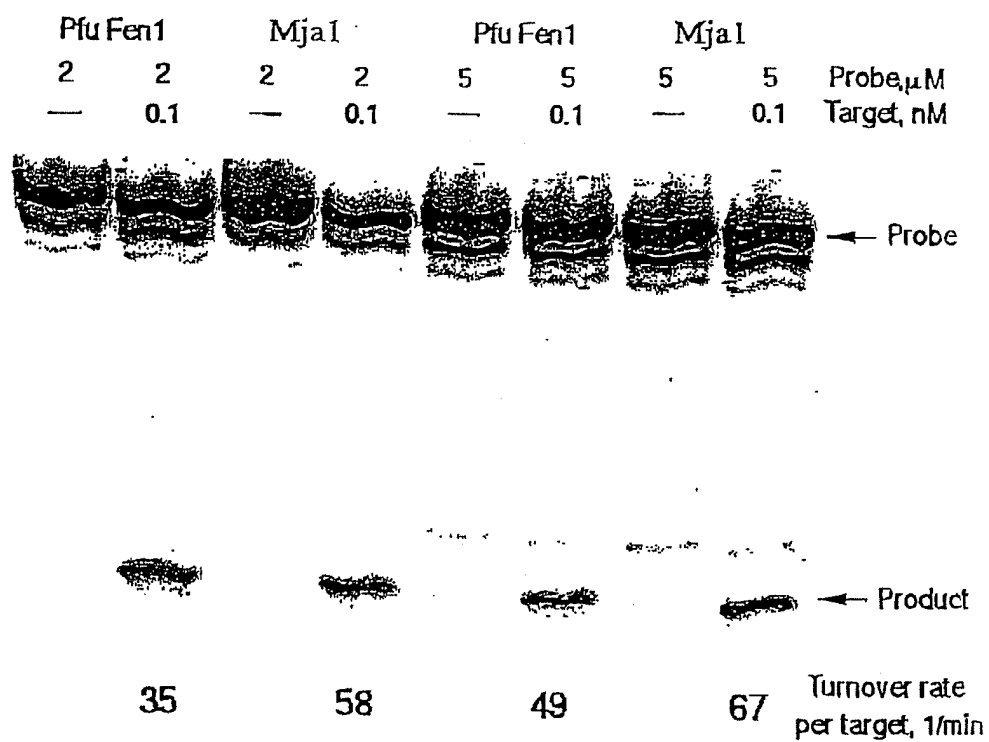
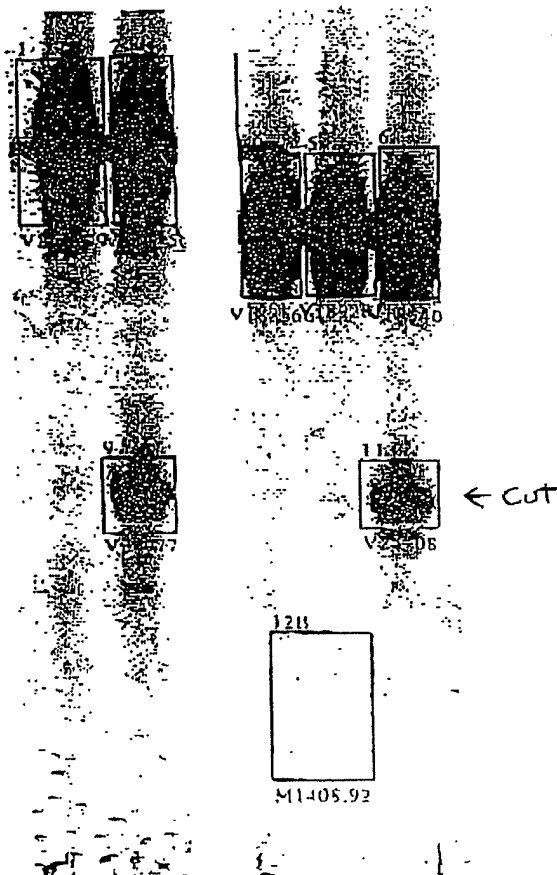
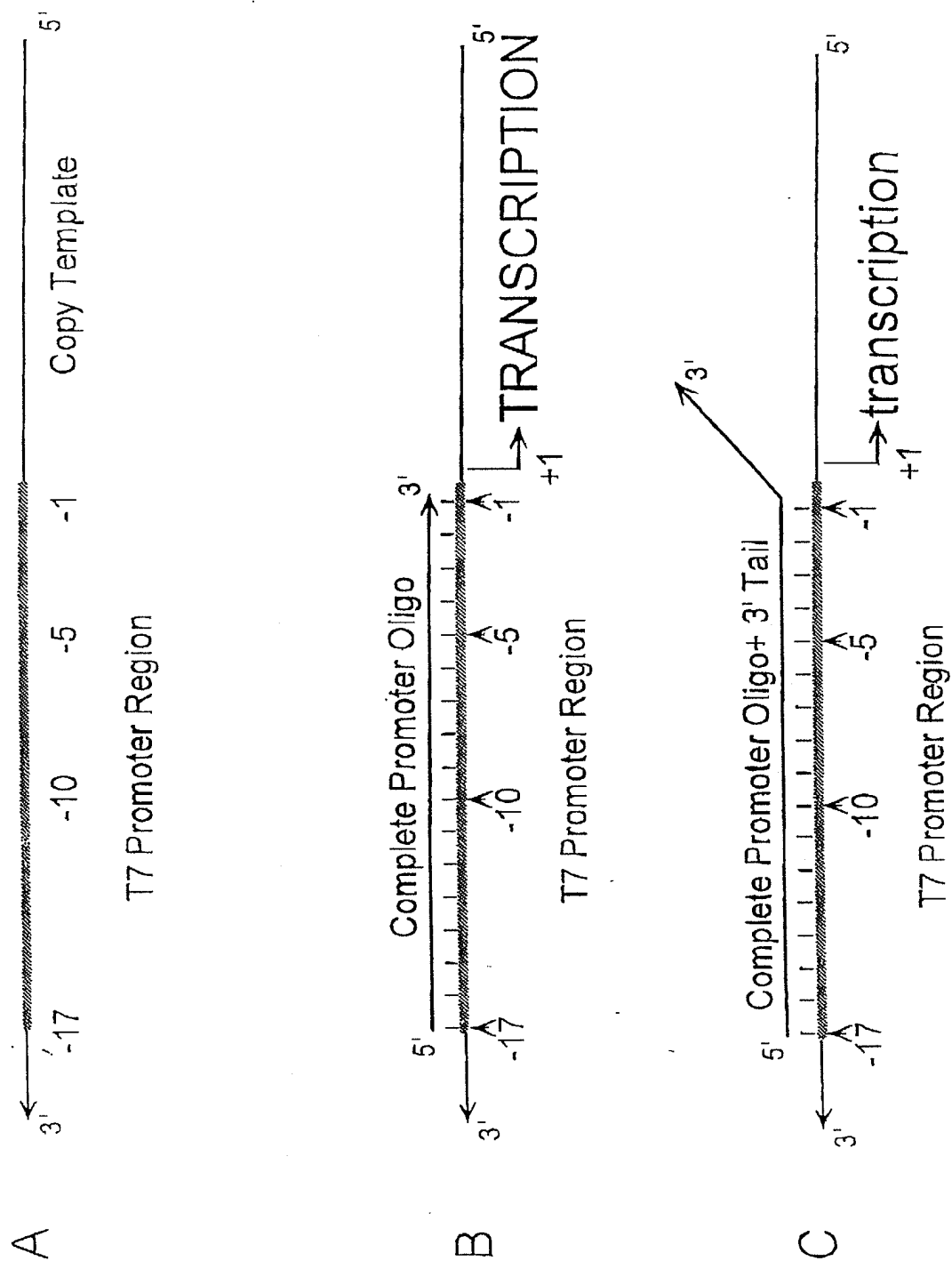


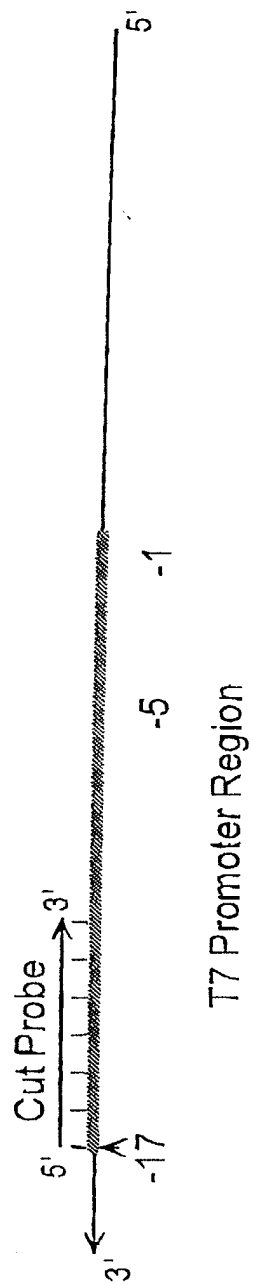
FIGURE 84

1 2 3 4 5

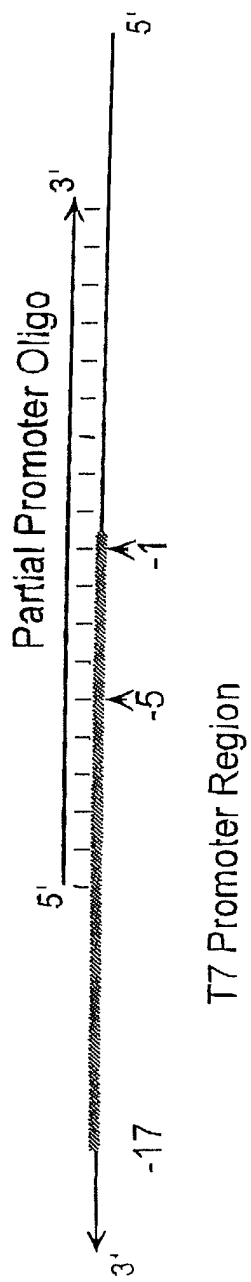


**FIGURE 85**



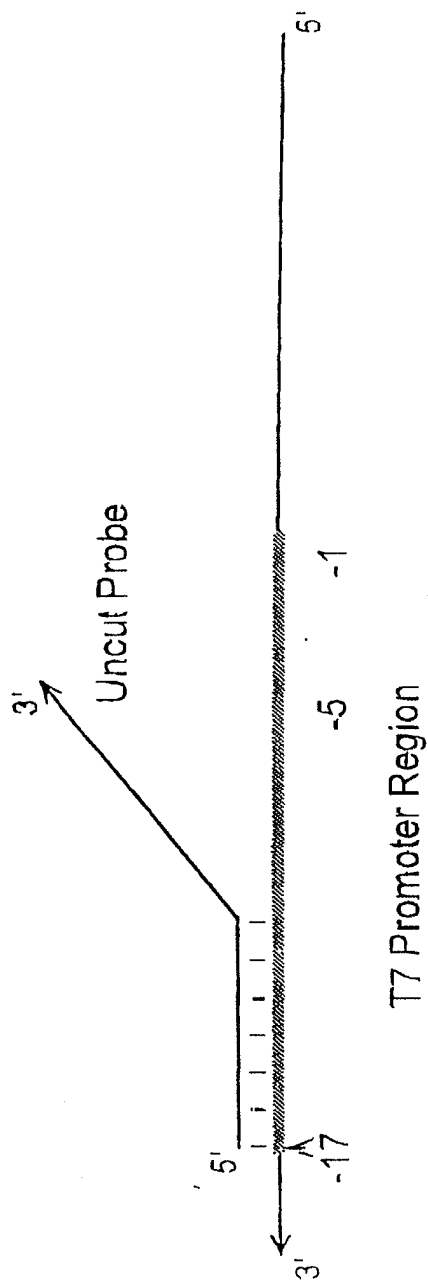


**FIGURE 86A**



**FIGURE 86B**

**FIGURE 86C**



**FIGURE 86D**

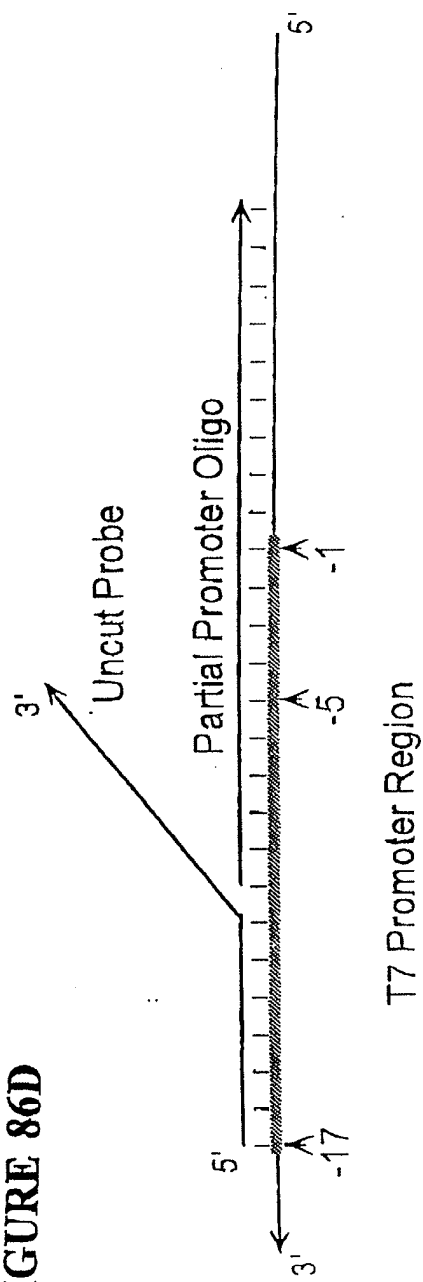


FIGURE 87

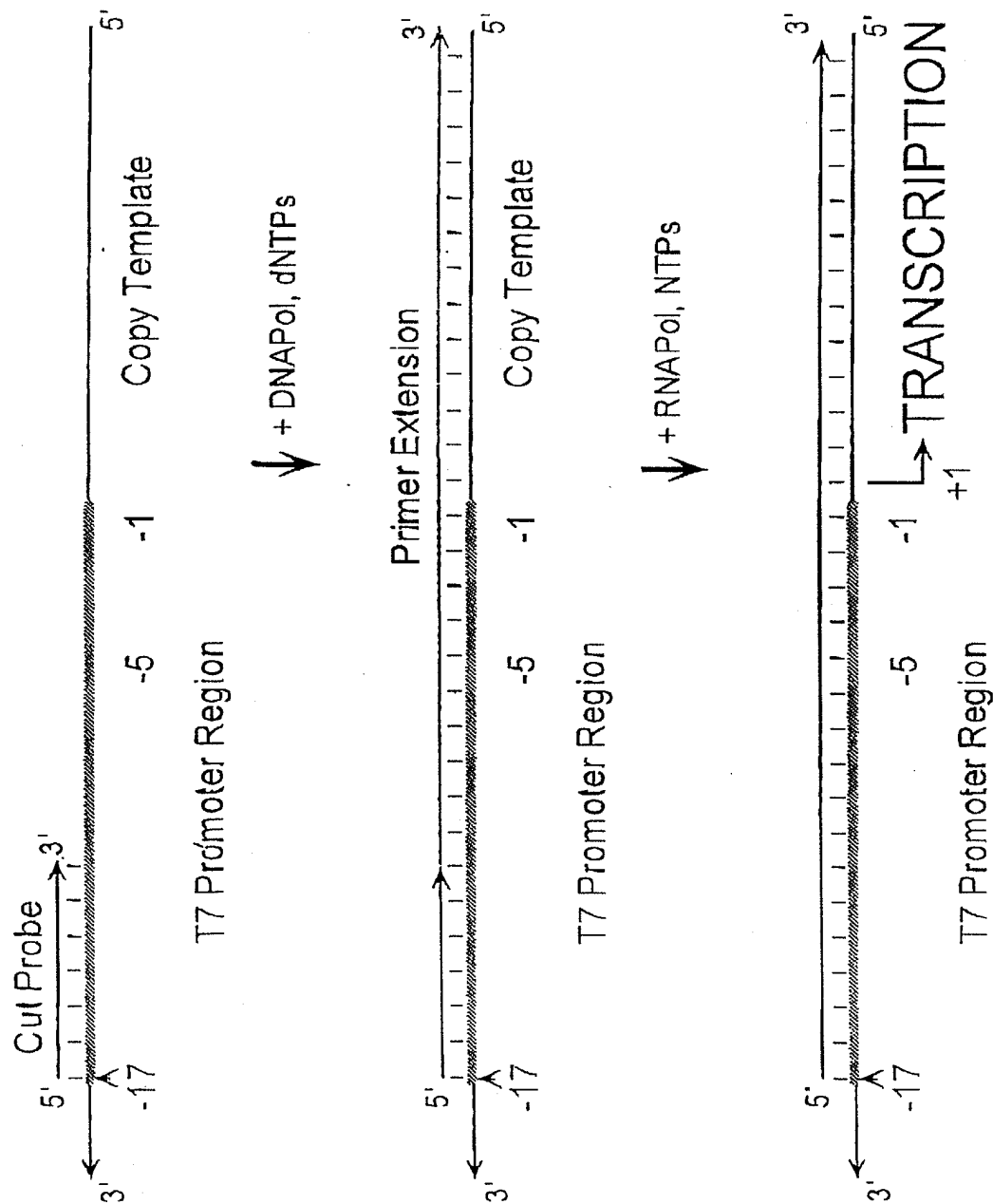




FIGURE 88A

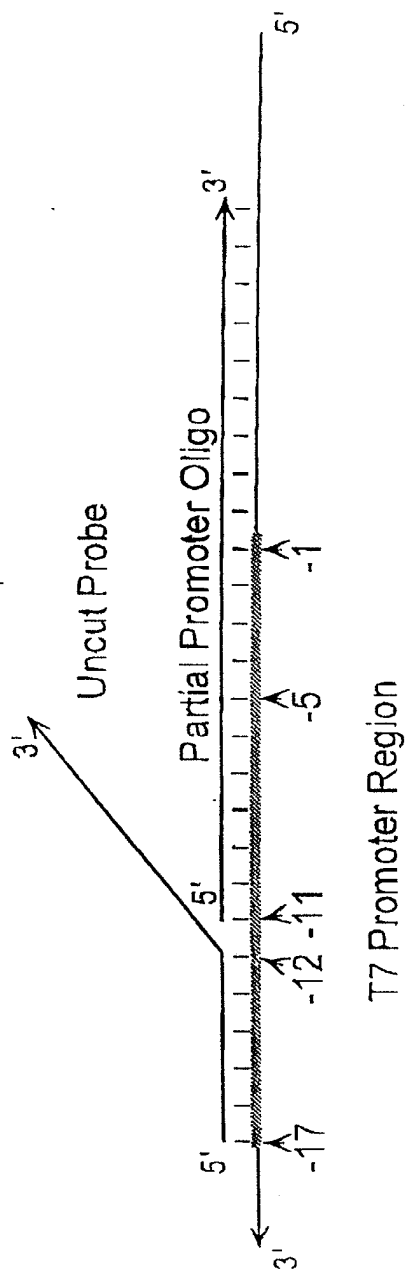


FIGURE 88B

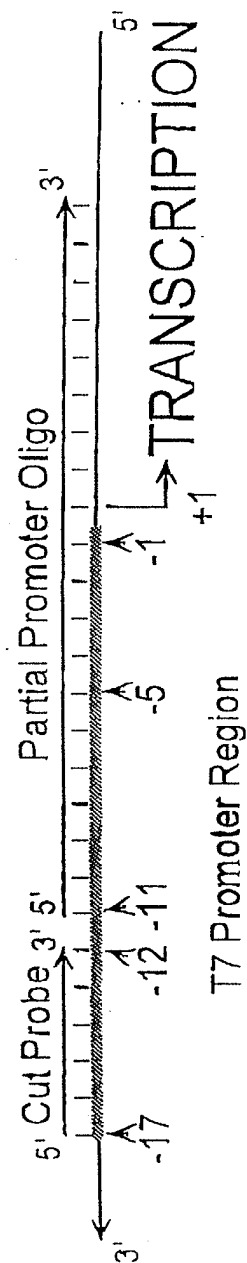


FIGURE 89

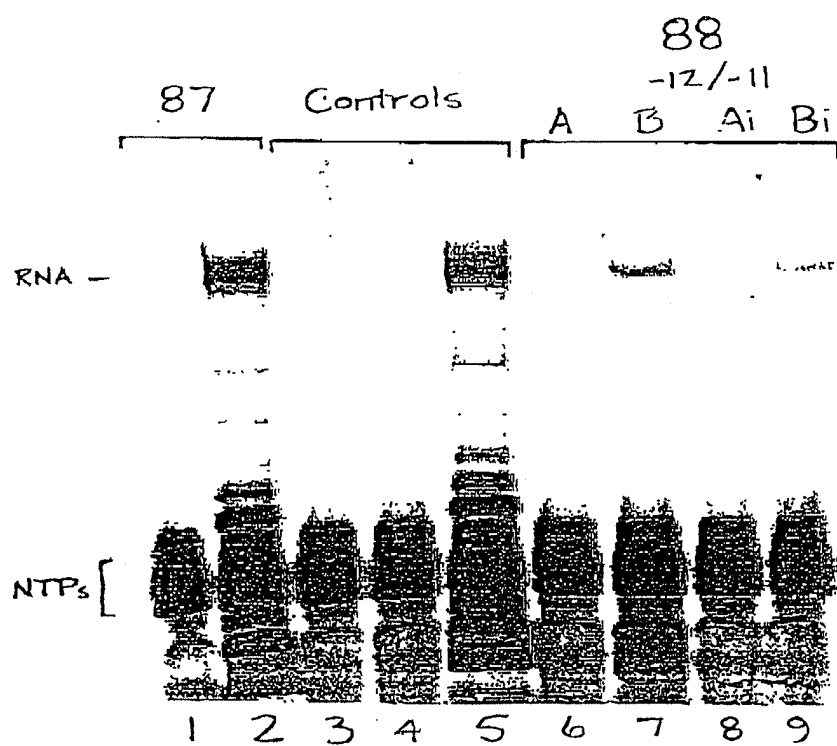
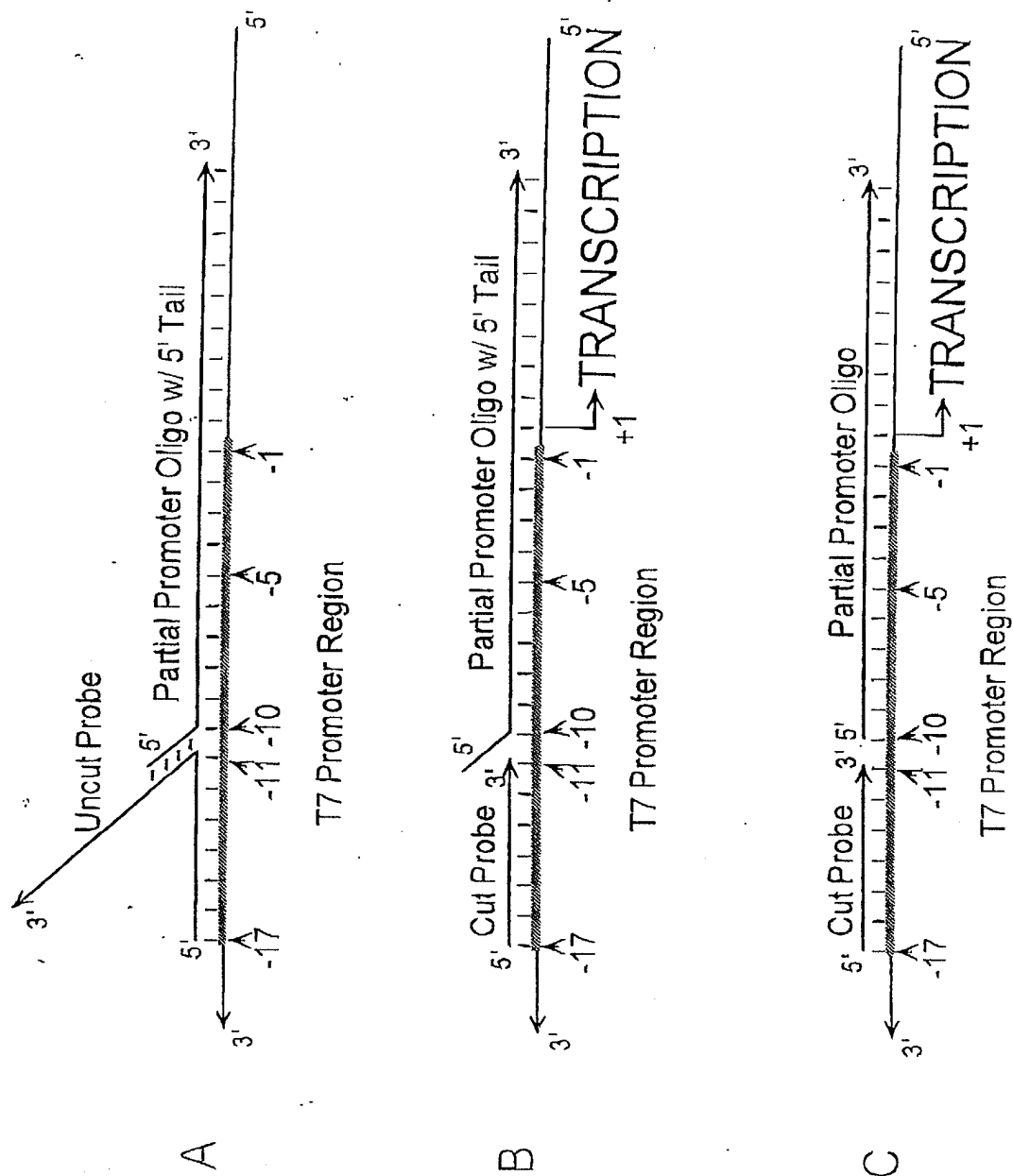
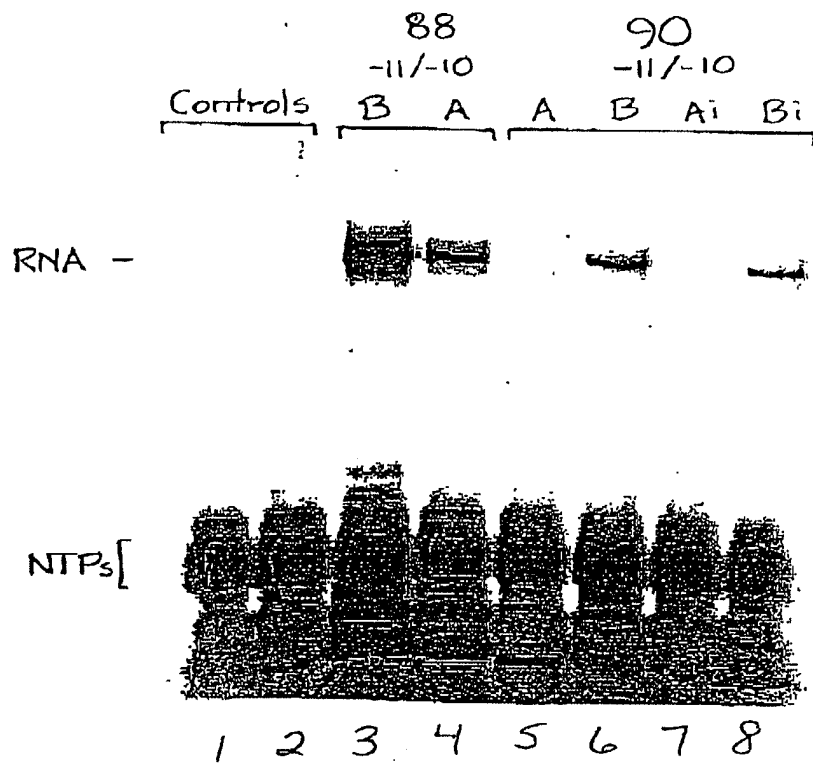


FIGURE 90





**FIGURE 91**

FIGURE 92

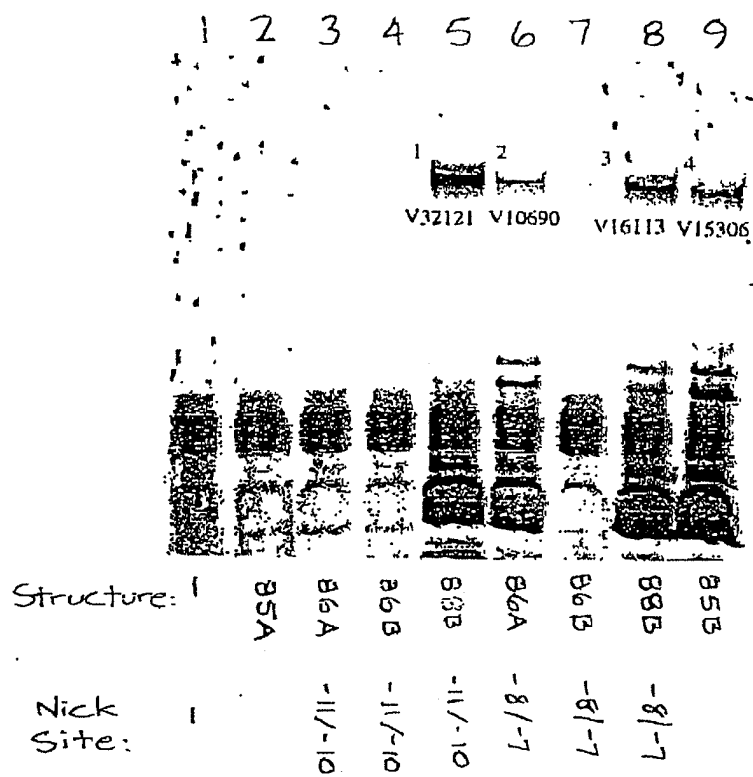


FIGURE 93

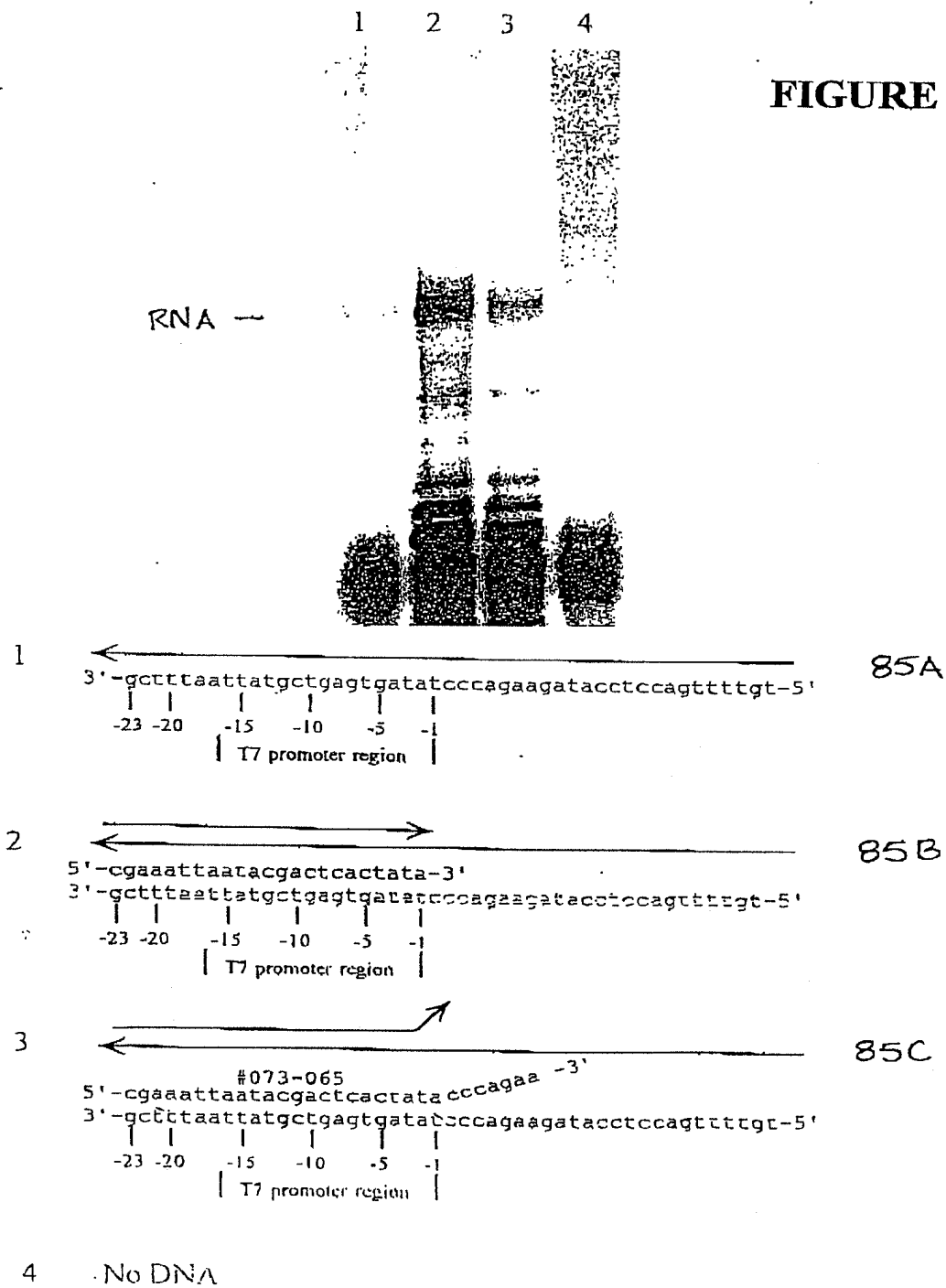
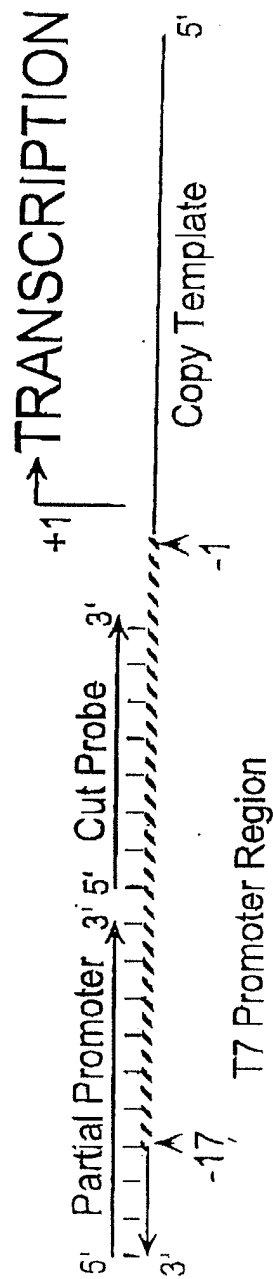
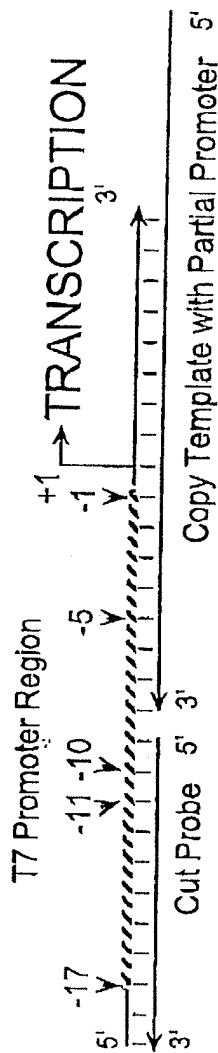


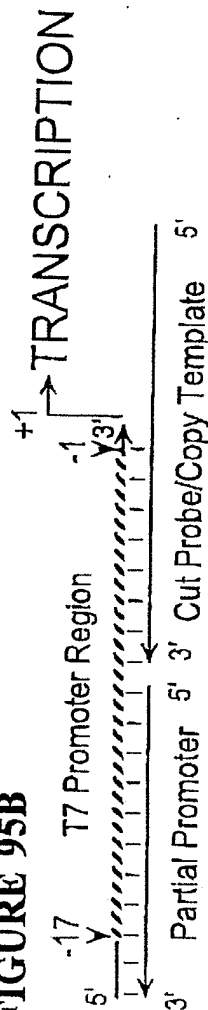
FIGURE 94



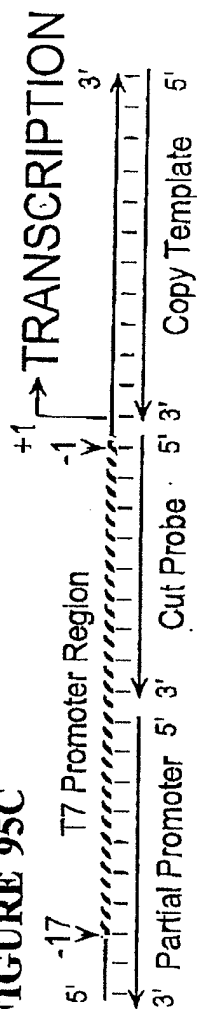
**FIGURE 95A**



**FIGURE 95B**



**FIGURE 95C**



**FIGURE 95D**

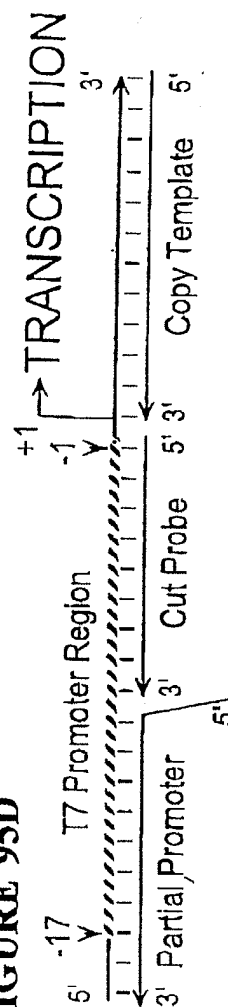




FIGURE 96

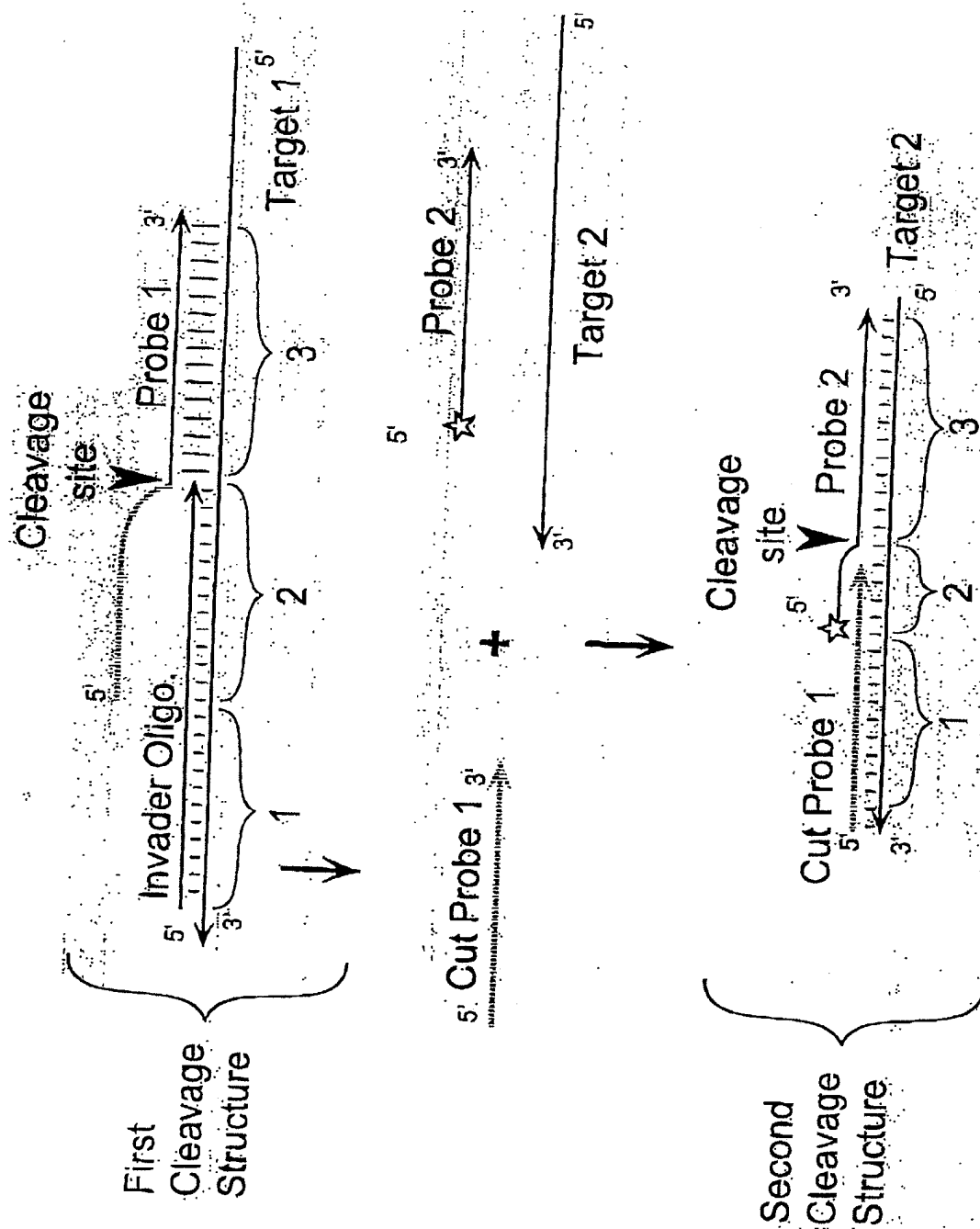


FIGURE 97

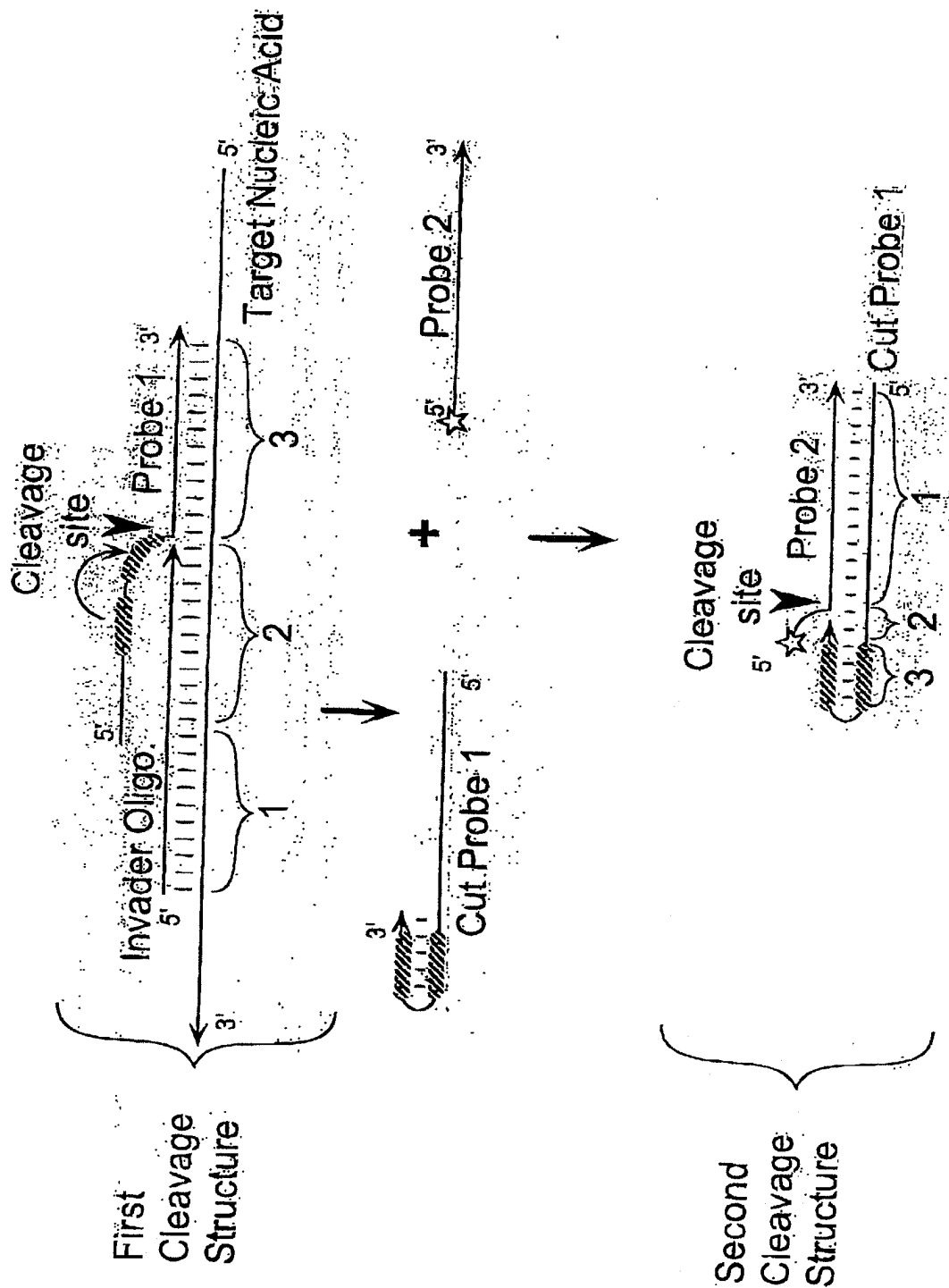


FIGURE 98

PR1 probe

Cleavage site

5'FITTITCCAGAGCCTAAT G3'

IT3 Invader-Target

A<sup>A</sup> ACGAGCGTCTTT G3'  
G TGCTCGCAGAAAGGTCTCGGATTAATTTTTTTTT5'

IT3-8 Invader-Target

A<sup>A</sup> AGCGTCTT G3'  
G TCGCAGAAGGTCTCGGATTAATTTTTTTTT5'

IT3-6 Invader-Target

A<sup>A</sup> CGTCTT G3'  
G GCAGAAGGTCTCGGATTAATTTTTTTTT5'

IT3-4 Invader-Target

A<sup>A</sup> ATCTT G3'  
G AGAAGGTCTCGGATTAATTTTTTTTT5'

IT3-3 Invader-Target

A<sup>A</sup> CTT G3'  
G GAAGGTCTCGGATTAATTTTTTTTT5'

IT3-0 Invader-Target

3'GAAGGTCTCGGATTAATTTTTTTTT5'

FIGURE 99

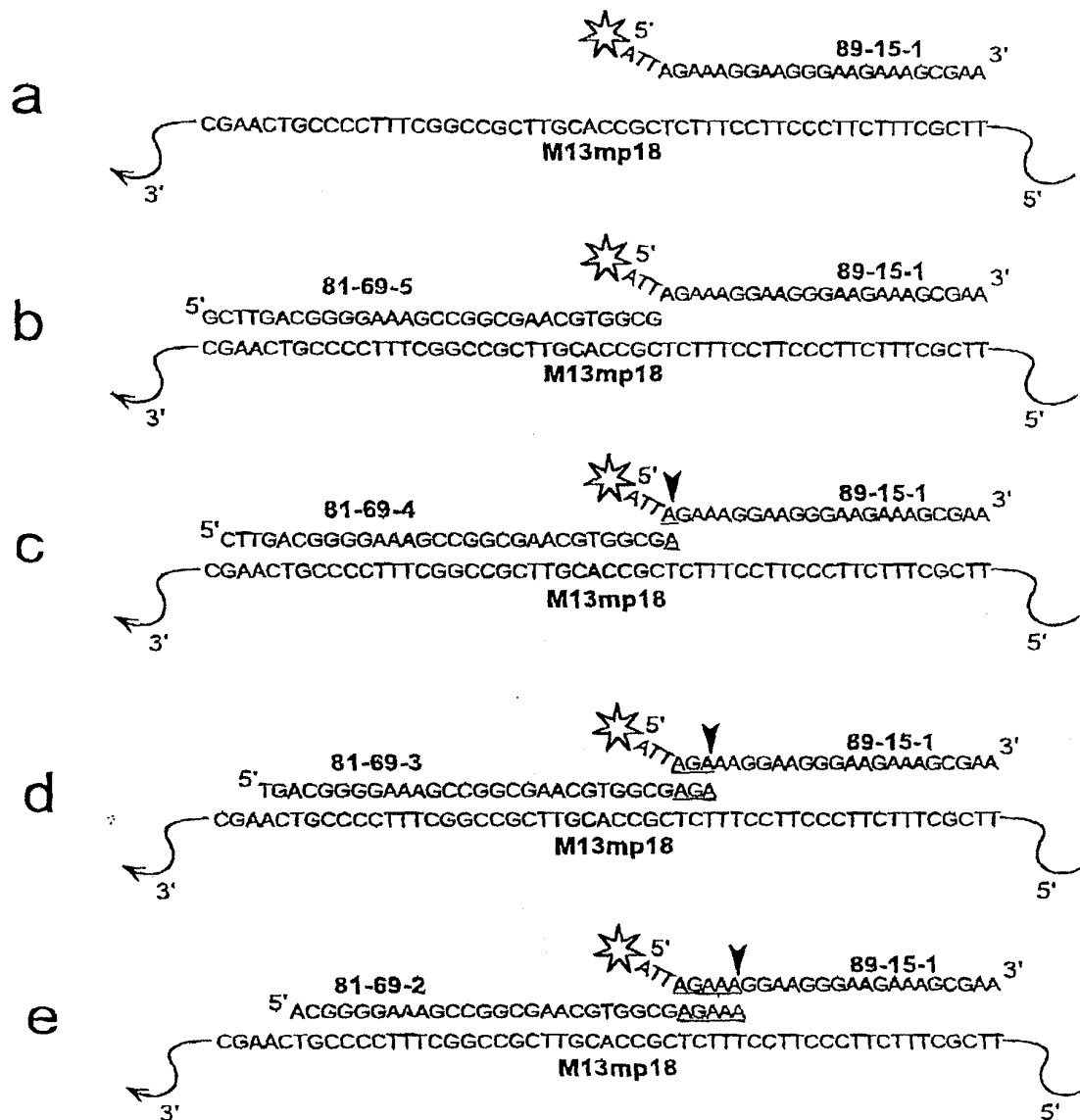


FIGURE 100

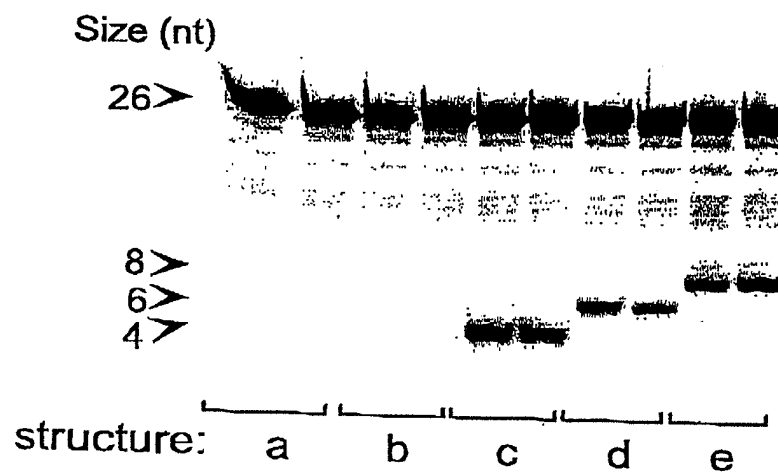


FIGURE 101

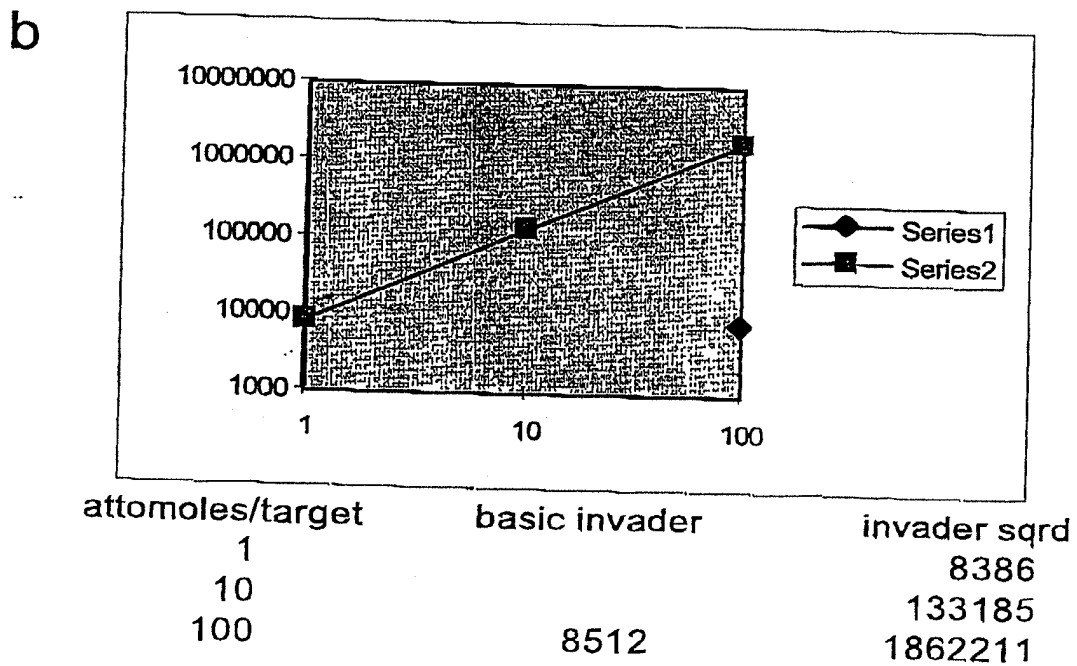
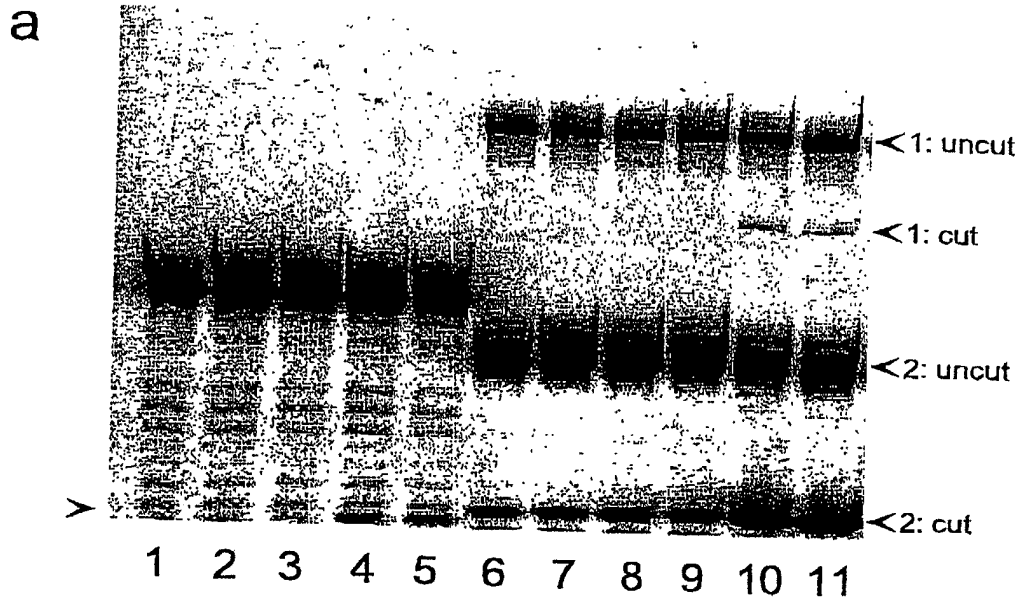


FIGURE 102

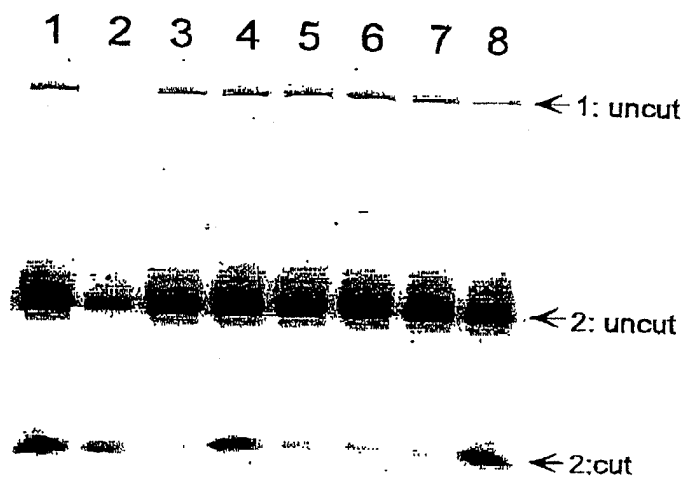


FIGURE 103

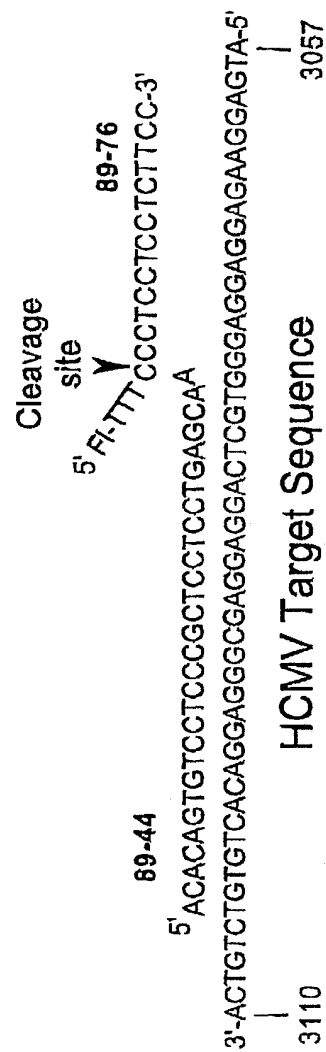




FIGURE 104

